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(54) Title: NUCLEIC ACIDS, PROTEINS, AND ANTIBODIES

(57) Abstract: The present invention relates to novel reproductive system related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "reproductive system related antigens", and the use of such reproductive system related antigens for detecting disorders of the reproductive system, particularly the presence of cancers and cancer metastases. More specifically, isolated reproductive system associated nucleic acid molecules are provided encoding novel reproductive system associated polypeptides. Novel reproductive system related polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human reproductive system associated polynucleotides and/or polypeptides. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the reproductive system, including reproductive system cancers, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting the production and function of the polypeptides of the present invention.

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

## Nucleic Acids, Proteins, and Antibodies

[001] This application refers to a "Sequence Listing" that is provided only on electronic media in computer readable form pursuant to Administrative Instructions Section 801(a)(i). The Sequence Listing forms a part of this description pursuant to Rule 5.2 and Administrative Instructions Sections 801 to 806, and is hereby incorporated in its entirety.

[002] The Sequence Listing is provided as an electronic file, (PC006PCT\_seqList.txt, 20,399,961 bytes in size, created on January 12, 2001) on four identical compact discs (CD-R), labeled "COPY 1," "COPY 2," "COPY 3," and "CRF." The Sequence Listing complies with Annex C of the Administrative Instructions, and may be viewed, for example, on an IBM-PC machine running the MS-Windows operating system by using the V viewer software, version 2000 (see World Wide Web URL: <http://www.fileviewer.com>).

### *Field of the Invention*

[003] The present invention relates to novel reproductive system related polynucleotides, the polypeptides encoded by these polynucleotides herein collectively referred to as "reproductive system antigens," and antibodies that immunospecifically bind these polypeptides, and the use of such reproductive system polynucleotides, antigens, and antibodies for detecting, treating, preventing and/or prognosing disorders of the reproductive system, including, but not limited to, the presence of cancer and cancer metastases. More specifically, isolated reproductive system nucleic acid molecules are provided encoding novel reproductive system polypeptides. Novel

reproductive system polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human reproductive system polynucleotides, polypeptides, and/or antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the reproductive system, including cancers of the reproductive system, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The invention further relates to methods and/or compositions for inhibiting or promoting the production and/or function of the polypeptides of the invention.

### ***Background of the Invention***

[004] The human reproductive system enables continuation of the species. Human beings reproduce sexually, require the involvement of both a male and a female. Reproduction involves the coalition of sex cells. A new human being begins its development after a sex cell (sperm), created by the male unites with a sex cell (ovum) created by the female. Both the male and female reproductive systems function through the complex interaction of several organs. Diseases or malfunctions of these organs can impair reproduction or cause infertility.

#### ***The Male Reproductive System***

[005] Male reproductive functions can be divided into three major subdivisions; spermatogenesis (the formation and maturation of sperm), performance of the male sexual act (arousal, erection, and ejaculation), and regulation of male sexual functions by the various hormones (mainly testosterone). Associated with these reproductive functions are the effects of the male sex hormones on the accessory sexual organs, cellular metabolism, growth, and on several other bodily functions. The onset of sexual maturation and these reproductive functions in males occurs at puberty, which, in humans, typically begins around age thirteen.

[006] The male reproductive system is composed of the testes, a pair of organs contained in the scrotum which include the seminiferous tubules and epididymus;



secretory glands, such as the prostate gland, seminal vesicles, bulbourethral glands, and urethral glands; tubular passageways, such as the vas deferens and urethra; and the penis, which functions in performance of the sexual act and sperm transmission.

- [007] Common disorders of the male reproductive system include infections, cancers, and inflammations of the above listed components, which are described in greater detail below.

#### *Disorders of the Testes*

- [008] The two primary functions of the testes are 1) production of testosterone and 2) production of sperm. Testosterone produced in the testes is released into the blood stream, where it travels to and acts on a wide range of tissues and organs within the male body. Disorders resulting from testosterone deficiency are manifested in the male reproductive system typically by symptoms of hypogonadism, which is the failure to go through puberty. Specifically, erectile function is impaired, and libido and sperm production are decreased or absent.

- [009] Known dysfunctions of sperm production include aspermia (the failure to produce an ejaculate), asthenospermia (the production of an ejaculate in which less than 50% of spermatozoa are motile), azoospermia (the production of an ejaculate devoid of spermatozoa), oligospermia (production of an ejaculate containing less than 20x100 spermatozoa per milliliter of semen), and teratospermia (the production of an ejaculate in which more than 50% of the spermatozoa are of abnormal shape), all of which result in impaired fertility. Improper sperm formation may result from a variety of factors, including congenital defects, genetic abnormalities, injury, and infection. For example, contraction of the mumps virus early in male adolescence can infect the testicles, leading to permanent complications in sperm production.

- [010] Sperm formation may also be impaired by disorders of the epididymus, the labyrinthine tube system located in each testis where sperm mature. Common disorders include infections (e.g., *Neisseria gonorrhoea*, *Pseudomonas*, *Enterobacteriaceae*, and *Chlamydia trachomatis*), cyst formation or other obstructions, and enlargement of the spermatoceles (liquid filled cavities in the epididymus).

- [011] During fetal development, the testes mature within the abdominal cavity and descend through the inguinal canal into the scrotum prior to birth. It is well known

that the testicles reside in the scrotum because it is cooler than other places within the body cavity, and even minor temperature differences can have a dramatic influence on the ability of the testicle to make sperm. An undescended testicle, sometimes called a cryptorchid testicle, is a fairly common problem in male babies. Typically, testicles undescended at birth will move into the scrotum within the first year of life, however in a small percentage of cases this migration does not occur. Early correction of this problem is crucial in preserving the fertility of the male, as the testicles begin to lose the ability to make sperm very early in life if they are not properly stored in the scrotum. Additionally, undescended testicles have a much higher rate of developing testicular cancer than testicles that descended spontaneously. Testicular cancer is the most common solid tumor in males aged 18 to 35. It typically is extremely aggressive and spreads early. A tumor of the testicle often shows itself by a fast enlargement of the testicle. Bringing the testes into the scrotum will allow for easier and more accurate examination of the testes, hopefully resulting in earlier detection of tumors. Further, undescended testicles are also associated with a greater risk of hernia.

[012] Disorders of the scrotal pouch commonly involve the small amount of fluid lining the pouch that allows for small movements and cushioning of the testicles. Several causes, such as testicular torsion, trauma, or tumors, may lead to an increase in the amount of liquid, causing the scrotal pouch to bulge. While this condition is harmless, it may cause irritation and discomfort if the bulge becomes too large.

[013] Another harmless, yet irritating disease of the testes is varicocele, a disorder of the small vein that runs the blood from the testicle back toward the heart. Small valves are present in these veins to prevent blood from flowing back toward the testicles. Sometimes, these valves malfunction, causing backflow and subsequent enlargement of the small vessel network in the scrotal sac. This gives rise to dull pain and an uncomfortable "bag of worms" feeling around the scrotum. There is currently considerable debate as to whether this phenomenon also contributes to decreased fertility.

#### *Disorders of the Vas Deferens and Seminal Vesicles*

[014] In the vas deferens, the sperm become mixed with a viscous, alkaline fluid from the seminal vesicles that constitutes 60% of semen. This fluid contains the

components for generating sperm motility and the enzymes necessary for fertilization of the egg within the female reproductive system. Disorders of the vas deferens and seminal vesicles are unusual, however a congenital defect where the vas deferens is absent is known to be associated with mutations in the CFTR gene, and a defect in seminal vesicle function is associated with the hydatid disease of the urogenital system.

#### *Disorders of the Prostate Gland*

[015] Disorders of the prostate gland are typically manifested by enlargement of the gland, leading to such symptoms as impaired urinary flow, infertility, and pain. For example, benign prostatic hyperplasia is the non-cancerous growth of the prostate gland, a condition that is fairly common in men over sixty. Prostate cancer, too, is extremely prevalent and is now the second most common type of cancer in males. Although men of any age can develop prostate cancer, it is found most frequently in men over age 50. Types of prostate cancers include, but not limited to, adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas. The prostate is subject to infections or inflammation, which may also result in enlargement of the prostate, such as acute bacterial prostatitis, chronic bacterial prostatitis, and nonbacterial prostatitis.

#### *Disorders of the Penis and Urethra*

[016] During sexual activity, the penis becomes rigid and erect, enabling penetration and deposition of sperm. An erection results from complex interaction of neurologic, vascular, hormonal, and psychologic actions. Several types of infections and inflammatory disorders can effect the penis and its function. Balanoposthitis is a generalized inflammation of the head of the penis (glans penis) and foreskin, commonly caused by a yeast or bacterial infection beneath the foreskin of an uncircumcised penis. Symptoms include pain, itching, redness, and swelling and can ultimately lead to a narrowing (stricture) of the urethra. Other infectious and inflammatory disorders, such as balanitis xerotica obliterans (a hardening of the tip of the penis which ultimately blocks urine and semen flow), phimosis (the shrinking or tightening of the foreskin), paraphimosis (inability of the retracted foreskin to be

pulled back over the head of the penis), and Erythroplasia of Queyrat (an infection causing a clearly defined reddish, velvety area on the skin of the penis). If left untreated, many of these infections may become cancerous.

[017] Other infections can lead to penile growths, such as the small painless sores associated with syphilis, tiny blisters from the herpes simplex virus, firm nodules from genital warts, and dimpled growths (molluscum contagiosum) from an unknown virus. Small sores and growths are also associated with skin cancers (e.g., squamous cell carcinoma, Bowen's disease, and Paget's disease) that can occur anywhere on the penis.

[018] The causes of the two major erectile disorders are not well understood. Priapism is a painful, persistent erection unaccompanied by sexual desire or excitement. In most cases, priapism is believed to stem from habitual drug use, but is had also been associated with blood disorders (e.g., blood clots, leukemia, or sickle cell disease), tumors in the pelvis or spine, and infection of the genitals. Peyronie's disease is manifested as a fibrous thickening of tissue that causes the penis to develop contractures so that the shape of an erection is distorted. The curvature of the erect penis can make sexual penetration difficult or impossible and may make erections extremely painful. Current therapies include corticosteroid injections, ultrasound treatments, or, more commonly, surgery, which may lead to impotence.

[019] Impotence, or erectile dysfunction, is the consistent or recurrent inability to attain and maintain a penile erection rigid enough for satisfactory sexual intercourse. Erectile dysfunction relates only to the erectile capability of the penis, excluding problems of libido, ejaculation, and orgasm. It is now accepted that the majority of cases have a physical and not a psychogenic root. Physical causes include anatomic deformations (e.g., malformed genitalia or penile injury), diabetes mellitus, coronary disease, hypertension, atherosclerosis, high cholesterol levels, multiple sclerosis, stroke, lower spine diseases, and rectal or prostate surgery.

### *The Female Reproductive System*

[020] The female reproductive system is comprised of both external and internal organs. The external organs function in permitting sperm to enter the body and protecting the internal genital organs from infection and injury. The internal organs

form a pathway (the genital tract) for reproduction, beginning at the ovaries, through the fallopian tubes (oviducts) and uterus, to the birth canal (vagina).

[021] The sexual and reproductive functions in the female can be divided into two major phases: first, preparation of the body for conception, and second, the gestation and parturition. Gestation and parturition only occur if an ovum becomes fertilized. If fertilization does not occur, the reproductive system undergoes a cycle to ensure frequent readiness for conception and fertilization.

[022] Common disorders of the female reproductive system include infections, cancers, and inflammations of the organs, which are described in greater detail below.

#### *Disorders of the Uterus*

[023] Disorders of the uterus include absent bleeding (amenorrhea) and abnormal bleeding. Amenorrhea is normal only before puberty, during pregnancy, while breastfeeding, and after menopause. The absence of menses at other times is considered aberrant and may be indicative of problems in the brain, pituitary gland, thyroid gland, adrenal glands, ovaries, or virtually any other part of the reproductive tract. For example, the hypothalamus signals the pituitary gland to release hormones that cause the ovaries to release eggs. Inappropriately low levels of hypothalamic hormones prevent egg release, halting the menstrual cycle. The same is true for the thyroid and adrenal glands. To illustrate, in Cushing's syndrome, excess production of cortisol by the adrenal glands causes periods to be absent or irregular. The absence of periods can also be caused by growths (e.g., hydatidiform moles) or scarring of the uterine lining due to infection or surgery (e.g., Asherman's syndrome).

[024] Some women do not undergo puberty at all - consequently their periods never start. Causes include a birth defect in which the uterus or fallopian tubes develop abnormally and chromosomal disorders. For example, in Turner's syndrome, the female was formed from a zygote containing only one X chromosome and shows reproductive abnormalities, such as amenorrhea and chronically immature breasts, labia, vagina.

[025] Premature menopause is also a condition resulting in amenorrhea. Menopause is considered abnormal when it occurs in women under the age of forty. Causes of premature menopause include genetic (usually chromosomal) abnormalities and

autoimmune disorders in which antibodies damage the ovaries. Estrogen replacement therapy can prevent or reverse the symptoms of menopause, however the chance of conceiving a child remains less than ten percent.

[026] Uterine bleeding is considered abnormal when it is atypically heavy, light, frequent, or irregular. Moreover, bleeding before puberty or after menopause is almost always abnormal. Uterine polyps, fibroids (noncancerous growths of muscle and fibrous tissues), and cancers are common causes of abnormal uterine bleeding and usually can be surgically removed. Cancers of the uterus include adenocarcinomas (cancers arising from the endometrial lining), leiomyosarcomas (cancers of the uterine smooth muscle), and sarcomas (cancers arising from the stroma).

[027] Aberrant bleeding resulting from hormonal irregularities (commonly referred to a dysfunctional uterine bleeding) occurs most frequently at the beginning and end of the reproductive years and typically results from sustained levels of estrogen. For example, in polycystic ovary syndrome the overproduction of luteinizing hormone stimulates the production of large amounts of androgens – some of which are converted to estrogen-which, without sufficient progesterone to counteract its effects, induces abnormal uterine bleeding.

[028] Endometriosis is a disorder of the uterus in which patches of endometrial tissue, which normally is found only in the uterine lining, grow outside the uterus. Because the misplaced tissue responds to the same hormone that the uterus responds to, it may bleed during the menstrual period, causing cramps, pain, irritation, and the formation of scar tissue. As the disease progresses, adhesions may form and block the functioning of organs.

[029] Disorders of uterine contraction include, for example, dysmenorrhea and pre-term labor. During a normal period, the uterus undergoes mild contractions in order to aid in blood flow. Dysmenorrhea results when the contractions become inappropriately strong, inhibiting blood flow to the uterus. This deprives uterine muscle of oxygen, causing severe abdominal pain, as well as nausea, vomiting, diarrhea, headaches, weakness, and/or fainting. Sever cases of dysmenorrhea can significantly disrupt a womans life, leading to heavy work/school absenteeism and cases of pain killer addiction. Pre-term labor is also aserious problem, resulting in a dramatic rise in associated infant morbidity and mortality (83% of infant deaths occur

in gestations less than 37 weeks). Therapies for extending the length of pregnancy beyond 32 weeks, and preferably beyond 36 weeks, could significantly reduce the incidence of neonatal morbidity and virtually eliminate a major cause of neonatal mortality.

### *Disorders of the Ovary*

[030] Anovulation (the absence of egg release by the ovaries) is a serious condition leading to infertility. The exact etiology of anovulation, especially in women with otherwise normal menstrual cycles, is unclear, however several potential causes are under study, including: impaired follicular development (probably due to low or absent estrogen production or binding), normal follicular development with lack of egg release (probably due to progesterone deficiency), or insufficient production of gonadotropin-releasing hormone from the hypothalamus. Current treatments include clomiphene injections or hormonal therapy, although both can lead to serious side effects such as ovarian cancer and ovarian hyperstimulation syndrome.

[031] Anovulation is also associated with polycystic ovary syndrome (also known as Stein-Leventhal syndrome). This syndrome is an endocrine disorder characterized by an elevated level of male hormones (androgens). Other than anovulation, symptoms include growth of male-patterned body hair (hirsutism), excessive acne, irregular or absent menses, excessive bleeding, and obesity. Usually, the ovaries appear enlarged and may contain many follicular cysts.

[032] Ovarian cancer develops most often in women between the ages of 50 and 70. It is the third most common cancer of the female reproductive system, but more women die of ovarian cancers than of any other. Ovaries include a variety of cell types, each of which may give rise to a distinct type of cancer, including, but not limited to, ovarian epithelial cancer, ovarian germ cell tumors, ovarian papillary serous adenocarcinoma, ovarian mucinous adenocarcinoma, ovarian Krukenberg tumor, malignant mixed Mullerian tumors, and ovarian low malignant tumors.

[033] Other disorders of the ovaries also include, but are not limited to, inflammatory disorders, such as oophoritis (e.g., caused by viral or bacterial infection), ovarian cysts, and autoimmune disorders (e.g., premature ovarian failure and autoimmune oophoritis).

*Disorders of the Vagina and Vulva*

[034] The vagina and vulva are self-cleaning. Secretions and discharges flow downward through the vagina and vulva, flushing out dead cells and other substances. Despite this cleaning mechanism, infections and inflammation are a common problem. The most common vaginal infections are bacterial vaginitis, candida vaginitis (e.g., yeast infections), trichomonas vaginitis, and vulvitis. Vaginal or vulvar itching, irritation, and abnormal discharge characterize all.

[035] Cancer of the vagina is extremely rare, accounting for only two percent of all gynecological cancers, and occurs primarily in women over the age of 50. The severity of the disease depends on the type of cancer and its exact location. Varieties include, for example, squamous cell carcinoma and clear cell adenocarcinoma. Once cancer appears in the vagina, it easily spreads to surrounding tissues. Vulvar cancer is equally unusual as vaginal, and is predominantly manifested as a form of skin cancer, e.g. squamous cell carcinomas and basal cell carcinomas. Other vulvar cancers include Paget's disease, cancer of Bartholin's gland, and melanomas. Unlike cancer of the vagina, vulvar cancers typically grow slowly and infrequently metastasize.

*Disorders of the Breast*

[036] Disorders of the breast typically involve the formation of lesions within breast tissue. While many of these lesions are benign in nature, they may lead to cancer if left untreated.

[037] Benign breast lesions include, for example, cysts, which are non-cancerous, fluid-filled sacs that form a mass within breast tissue. The cause of breast cysts is unknown, though injury may be involved, and their main symptom is pain. While considered harmless, a professional should drain cysts and the fluid examined because cancer of the cyst wall, although quite rare, is possible.

[038] Other benign breast lesions include fibrous breast lumps (fibroadenomas), breast infection (mastitis), intraductal papilloma, and abscesses. Fibrous breast lumps are small, solid lumps of glandular tissue. These lumps usually appear in young women, often in teenagers, and are easy to remove. Intraductal papilloma are small lumps located within a milk duct, often causing inappropriate discharge from the



nipple. Breast abscesses are collections of pus in breast tissue that develop from breast infections that go untreated.

[039] Breast cancer is the most common cancer among women, other than skin cancer and is the second leading cause of cancer death in women, after lung cancer. The American Cancer Society predicts that there will be about 182,800 new cases of invasive breast cancer in the year 2000 among women in this country and about 40,800 deaths from the disease. Breast cancer also occurs among men, although much less often. It is generally believed that this malignancy arises from a multi step process involving mutations in a relatively small number of genes, perhaps 10 or less. These mutations result in significant changes in the growth and differentiation of breast tissue that allow it to grow independent of normal cellular controls, to metastasize, and to escape immune surveillance. The genetic heterogeneity of most breast cancers suggests that they arise by a variety of initiating events and that the characteristics of individual cancers are due to the collective pattern of genetic changes that accumulate.

[040] The discovery of new human reproductive system associated polynucleotides, the polypeptides encoded by them, and antibodies that immunospecifically bind these polypeptides, satisfies a need in the art by providing new compositions which are useful in the diagnosis, treatment, prevention and/or prognosis of disorders of the reproductive system, including, but not limited to, disorders of the male reproductive system including, for example, testicular disorders (e.g., hypogonadism, infection (e.g., *Neisseria gonorrhoea*, Enterobacteriaceae, and/or as described in the "Reproductive System Disorders" section below), asthenospermia, teatospermia, cryptorchid testicle, testicular cancers, varicocele, and/or as described in the "Reproductive System Disorders" section below), prostate disorders (e.g., prostate cancers, benign prostatic hyperplasia, and/or as described in the "Reproductive System Disorders" section below), disorders of the penis (e.g., balanoposthitis, phimosis, genital warts, skin cancer, priapism, Peyronie's disease, erectile dysfunction, and/or as described in the "Reproductive System Disorders" section below); and disorders of the female reproductive system including, for example, disorders of the uterus (e.g., Cushing's syndrome, Asherman's syndrome, Turner's syndrome, premature menopause, uterine cancers, endometriosis, and/or as described in the "Reproductive System Disorders" section below), ovarian disorders (e.g., anovulation, polycystic ovary syndrome,

ovarian cancers, and/or as described in the "Reproductive System Disorders" section below), vaginal and vulvar disorders (e.g., vulvitis, vaginal infections, Paget's disease, cancers of the vagina and vulva, and/or as described in the "Reproductive System Disorders" section below), and breast disorders (e.g., breast cancers, fibroadenomas, intraductal papillomas, and/or as described in the "Reproductive System Disorders" section below).

### *Summary of the Invention*

[041] The present invention relates to novel reproductive system related polynucleotides, the polypeptides encoded by these polynucleotides herein collectively referred to as "reproductive system antigens," and antibodies that immunospecifically bind these polypeptides, and the use of such reproductive system polynucleotides, antigens, and antibodies for detecting, treating, preventing and/or prognosing disorders of the reproductive system, including, but not limited to, the presence of cancer and cancer metastases. More specifically, isolated reproductive system nucleic acid molecules are provided encoding novel reproductive system polypeptides. Novel reproductive system polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human reproductive system polynucleotides, polypeptides, and/or antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the reproductive system, including cancers of the reproductive system, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The invention further relates to methods and/or compositions for inhibiting or promoting the production and/or function of the polypeptides of the invention.

### *Detailed Description*

#### Tables

[042] Table 1A summarizes some of the polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) and contig nucleotide sequence identifier (SEQ ID NO:X)) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby. The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA plasmid related to each reproductive system associated contig sequence disclosed in Table 1A. The second column provides a unique contig identifier, "Contig ID:" for each of the contig sequences disclosed in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for each of the contig polynucleotide sequences disclosed in Table 1A. The fourth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:X that delineate the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A as SEQ ID NO:Y (column 5). Column 6 lists residues comprising predicted epitopes contained in the polypeptides encoded by each of the preferred ORFs (SEQ ID NO:Y). Identification of potential immunogenic regions was performed according to the method of Jameson and Wolf (CABIOS, 4:181-186 (1988)); specifically, the Genetics Computer Group (GCG) implementation of this algorithm, embodied in the program PEPTIDESTRUCTURE (Wisconsin Package v10.0, Genetics Computer Group (GCG), Madison, Wisc.). This method returns a measure of the probability that a given residue is found on the surface of the protein. Regions where the antigenic index score is greater than 0.9 over at least 6 amino acids are indicated in Table 1A as "Predicted Epitopes." In particular embodiments, reproductive system associated polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the predicted epitopes described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. Column 7, "Tissue Distribution" shows the expression profile of tissue, cells, and/or cell line libraries which express the polynucleotides of the invention. The first

number in column 7 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. Expression of these polynucleotides was not observed in the other tissues and/or cell libraries tested. For those identifier codes in which the first two letters are not "AR", the second number in column 7 (following the colon), represents the number of times a sequence corresponding to the reference polynucleotide sequence (e.g., SEQ ID NO:X) was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of <sup>33</sup>P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression. Column 8, "Cytologic Band," provides the chromosomal location of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian

Inheritance in Man, OMIM™. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). If the putative chromosomal location of the Query overlapped with the chromosomal location of a Morbid Map entry, an OMIM identification number is provided in Table 1A, column 9 labeled "OMIM Disease Reference(s)". A key to the OMIM reference identification numbers is provided in Table 5.

[043] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

[044] Table 2 summarizes homology and features of some of the polypeptides of the invention. The first column provides a unique clone identifier, "Clone ID NO:Z", corresponding to a cDNA disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" corresponding to contigs in Table 1A and allowing for correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide sequences. The fourth column provides the analysis method by which the homology/identity

disclosed in the row was determined. Comparisons were made between polypeptides encoded by the polynucleotides of the invention and either a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFAM") as further described below. The fifth column provides a description of PFAM/NR hits having significant matches to a polypeptide of the invention. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in column five. Columns 8 and 9, "NT From" and "NT To" respectively, delineate the polynucleotides in "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth column. In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, an amino acid sequence encoded by the polynucleotides in SEQ ID NO:X as delineated in columns 8 and 9, or fragments or variants thereof.

[045] Table 3 provides polynucleotide sequences that may be disclaimed according to certain embodiments of the invention. The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to reproductive system associated contig sequences disclosed in Table 1A. The second column provides the sequence identifier, "SEQ ID NO:X", for contig polynucleotide sequences disclosed in Table 1A. The third column provides the unique contig identifier, "Contig ID", for contigs disclosed in Table 1A. The fourth column provides a unique integer 'a' where 'a' is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, represented as "Range of a", and the fifth column provides a unique integer 'b' where 'b' is any integer between 15 and the final nucleotide of SEQ ID NO:X, represented as "Range of b", where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. For each of the polynucleotides shown as SEQ ID NO:X, the uniquely defined integers can be substituted into the general formula of a-b, and used to describe polynucleotides which may be preferably excluded from the invention. In certain embodiments, preferably excluded from the polynucleotides of the invention (including polynucleotide fragments and variants as described herein and diagnostic and/or therapeutic uses based on these polynucleotides) are at least one, two, three, four, five, ten, or more of the polynucleotide sequence(s) having the accession number(s) disclosed in the sixth

column of this Table (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone).

[046] Table 4 provides a key to the tissue/cell source identifier code disclosed in Table 1A, column 7. Column 1 provides the key to the tissue/cell source identifier code disclosed in Table 1A, Column 7. Columns 2-5 provide a description of the tissue or cell source. Codes corresponding to diseased tissues are indicated in column 6 with the word "disease". The use of the word "disease" in column 6 is non-limiting. The tissue or cell source may be specific (e.g. a neoplasm), or may be disease-associated (e.g., a tissue sample from a normal portion of a diseased organ). Furthermore, tissues and/or cells lacking the "disease" designation may still be derived from sources directly or indirectly involved in a disease state or disorder, and therefore may have a further utility in that disease state or disorder. In numerous cases where the tissue/cell source is a library, column 7 identifies the vector used to generate the library.

[047] Table 5 provides a key to the OMIM<sup>TM</sup> reference identification numbers disclosed in Table 1A, column 9. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM<sup>TM</sup>. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine, (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). Column 2 provides diseases associated with the cytologic band disclosed in Table 1A, column 8, as determined from the Morbid Map database.

[048] Table 6 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

[049] Table 7 shows the cDNA libraries sequenced, tissue source description, vector information and ATCC designation numbers relating to these cDNA libraries.

[050] Table 8 provides a physical characterization of clones encompassed by the invention. The first column provides the unique clone identifier, "Clone ID NO:Z",

for certain cDNA clones of the invention, as described in Table 1A. The second column provides the size of the cDNA insert contained in the corresponding cDNA clone.

### Definitions

[051] The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

[052] In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide sequences of the present invention.

[053] As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence encoding SEQ ID NO:Y or a fragment or variant thereof, a nucleic acid sequence contained in SEQ ID NO:X (as described in column 3 of Table 1A) or the complement thereof, a cDNA sequence contained in Clone ID NO:Z (as described in column 1 of Table 1A and contained within a library deposited with the ATCC); a nucleotide sequence encoding the polypeptide encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or a fragment or variant thereof; or a nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereof. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide



sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

[054] As used herein, a "reproductive system antigen" refers collectively to any polynucleotide disclosed herein (e.g., a nucleic acid sequence contained in SEQ ID NO:X or the complement thereof, or cDNA sequence contained in Clone ID NO:Z, or a nucleotide sequence encoding the polypeptide encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B, or a nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereof and fragments or variants thereof as described herein) or any polypeptide disclosed herein (e.g., an amino acid sequence contained in SEQ ID NO:Y, an amino acid sequence encoded by SEQ ID NO:X, or the complement thereof, an amino acid sequence encoded by the cDNA sequence contained in Clone ID NO:Z, an amino acid sequence encoded by SEQ ID NO:B, or the complement thereof, and fragments or variants thereof as described herein). These reproductive system antigens have been determined to be predominantly expressed in reproductive system tissues, including normal or diseased tissues (as shown in Table 1A column 7 and Table 4).

[055] In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown, for example, in column 1 of Table 1A, each clone is identified by a cDNA Clone ID (identifier generally referred to herein as Clone ID NO:Z). Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. Furthermore, certain clones disclosed in this application have been deposited with the ATCC on October 5, 2000, having the ATCC designation numbers PTA 2574 and PTA 2575; and on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 7 provides a list of the deposited cDNA libraries. One can use the Clone ID NO:Z to determine the library source by reference to Tables 6 and 7. Table 7 lists the deposited cDNA libraries by name and links each library to an ATCC

Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone (Clone ID NO:Z) isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1A correlates the Clone ID NO:Z names with SEQ ID NO:X. Thus, starting with an SEQ ID NO:X, one can use Tables 1A, 6 and 7 to determine the corresponding Clone ID NO:Z, which library it came from and which ATCC deposit the library is contained in. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

[056] In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5 kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

[057] A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), the polynucleotide sequence delineated in columns 8 and 9 of Table 2 or the complement thereof, and/or cDNA sequences contained in Clone ID NO:Z (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments, or the cDNA clone within the pool of cDNA clones deposited with the ATCC, described herein) and/or the polynucleotide sequence delineated in column 6 of Table 1B or the complement thereof. "Stringent hybridization conditions" refers to an overnight incubation at 42

degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

[058] Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency), salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M  $\text{NaH}_2\text{PO}_4$ ; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

[059] Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

[060] Of course, a polynucleotide which hybridizes only to polyA<sup>+</sup> sequences (such as any 3' terminal polyA<sup>+</sup> tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

[061] The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-

stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

[062] The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing,

phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992).)

[063] "SEQ ID NO:X" refers to a polynucleotide sequence described, for example, in Tables 1A or 2, while "SEQ ID NO:Y" refers to a polypeptide sequence described in column 5 of Table 1A. SEQ ID NO:X is identified by an integer specified in column 3 of Table 1A. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. "Clone ID NO:Z" refers to a cDNA clone described in column 1 of Table 1A.

[064] "A polypeptide having biological activity" refers to a polypeptide exhibiting activity similar to, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

[065] Table 1A summarizes some of the reproductive system associated polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and clones (Clone ID NO:Z) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby.

### **Polynucleotides and Polypeptides**

TABLE 1A

Clone ID NO: Z	Contig ID:	SEQ ID NO: X	ORF (From-To)	AA SEQ ID NO: Y	Predicted Epitopes	Tissue Distribution Library code: count (see Table IV for Library Codes)	Cytologic Band	OMIM Disease Reference(s):
H7MCE35	928554	11	71 - 3	2698		S0286: 1 and S0284: 1.		
H7MDC49	722780	12	125 - 3	2699		S0284: 2 and L0758: 1.		
H7MDD72	847688	13	100 - 510	2700	Glu-9 to Gly-22, Lys-50 to Lys-69, Gly-91 to Arg-107, Pro-113 to Ile-129, Tyr-131 to Gln-137.	AR054: 6, AR050: 2, AR051: 1, AR089: 1, AR061: 0 S0284: 2		
HAOSH55	887805	2651	3 - 824	5338				
	952380	14	2 - 355	2701	Pro-17 to Glu-28, Gly-86 to Ser-92.	L0770: 3, H0686: 1, H0634: 1, L0761: 1, L0772: 1, L0764: 1, L0805: 1, L0786: 1 and L0779: 1.		
HAQAK73	764671	15	449 - 661	2702	Glu-16 to Pro-21, Leu-28 to Asp-34, Glu-39 to Ser-56, Glu-59 to Gly-67.	H0295: 2 and L0748: 2.		
HAQAM17	664979	16	1 - 198	2703		H0295: 1 and H0435: 1.		
HAQBF84	783259	17	2 - 70	2704		H0295: 2		
HAQBJ71	839982	18	17 - 367	2705	Ala-55 to Phe-72.	H0295: 3 and H0294: 1.		
HAQBQ50	522004	19	3 - 59	2706		H0295: 2		

HAQBS37	847519	20	159 - 437	2707			H0295: 2, L0649: 1, L0663: 1, H0435: 1 and H0670: 1.		
HAUBD69	529711	21	3 - 134	2708			H0294: 2 and H0435: 1.		
HAUBU10	968339	22	209 - 337	2709			H0294: 2		
HBCJS08	957826	23	228 - 374	2710		Val-17 to Thr-27.	H0664: 2		
HBCPD14	963634	24	15 - 140	2711			H0663: 1 and S0152: 1.		
HBCQJ03	922401	25	138 - 1	2712		Arg-1 to Trp-15.	H0663: 2		
HBCQS90	951787	26	3 - 317	2713		Glu-24 to Lys-29, Lys-35 to Gln-40.	H0663: 2, L0758: 2, L0748: 1 and L0591: 1.		
HBCQS93	930682	27	390 - 575	2714		Gly-1 to Gly-6, Gly-41 to Pro-46.	L0749: 2, H0663: 1, H0662: 1 and L0438: 1.		
HBGBD28	525846	28	3 - 185	2715		Asn-37 to Gly-44.	H0181: 2		
HBGBF56	957870	29	2 - 184	2716		Pro-31 to Glu-36:	H0181: 1 and H0617: 1.		
HBGBG42	922396	30	1 - 420	2717			H0662: 2, H0181: 2, L0766: 2, L0455: 1, L0740: 1, L0779: 1 and L0362: 1.		
HBGBH43	524532	31	1 - 195	2718			H0553: 2, H0181: 2, L0743: 2, L0639: 1, L0787: 1, L0790: 1, L0747: 1, L0780: 1, L0752: 1 and L0755: 1.		
HBGBS07	954299	32	1 - 324	2719		Val-57 to Leu-66, Val-79 to Gly-84.	H0181: 2	1q21	104770, 107670, 110700, 135940,

HBGBT79	525352	33	109 - 306	2720	Arg-7 to Trp-17.	H0181: 2	145001, 146790, 152445, 152445, 159001, 174000, 179755, 182860, 182860, 182860, 191315, 230800, 230800, 266200, 600897, 601105, 601412, 601652, 602491
HBGBW60	954916	34	52 - 492	2721		H0617: 2 and H0181: 1.	
HBGBW72	524956	35	31 - 156	2722	Glu-1 to Gly-9.	H0181: 2 and H0617: 1.	
HBGDA44	525618	36	163 - 507	2723	Thr-1 to Pro-6.	H0181: 2	
HBGDE85	524875	37	1 - 132	2724	Pro-6 to Leu-12.	H0181: 2	
HBGDS13	971696	38	122 - 259	2725		H0181: 1 and H0617: 1.	
HBGDT43	974223	39	2 - 220	2726	Trp-8 to Gln-20.	H0181: 3	
HBGFA62	954306	40	3 - 302	2727	Gln-19 to Glu-24,	L0040: 1, H0188: 1,	



							Arg-29 to Pro-35, Ser-47 to Ser-56, Pro-58 to Ser-64.	H0606: 1, L0762: 1, L0803: 1, L0774: 1 and L0509: 1.		
HBGMD05	870189	41	266 - 589	2728			Thr-1 to Ser-6, Thr-23 to Pro-30.	H0617: 2		
HBGMD62	933763	42	84 - 329	2729			Leu-36 to Asn-42.	H0617: 3		
HBGMF10	966132	43	162 - 434	2730			Pro-13 to Ser-19, Pro-60 to Ala-76, Asp-78 to Gly-85.	L0764: 2, L0783: 2, H0182: 1, H0617: 1, H0616: 1, L0765: 1, L0375: 1, L0659: 1, L0809: 1, L0663: 1, L0731: 1 and L0361: 1.		
HBGMDG29	845194	44	22 - 279	2731			Arg-71 to Arg-76.	H0617: 2		
HBGMZ39	947112	45	575 - 3	2732			Arg-37 to Phe-48, Asp-55 to Asp-63, Gly-73 to Ala-80, Gln-147 to Trp-154, Val-176 to Lys-191.	AR089: 15, AR061: 10 H0617: 8, L0763: 2, L0754: 2, H0483: 1 and L0743: 1.		
HBGNA08	958257	46	82 - 162	2733				H0617: 2		
HBGND09	848219	47	1 - 522	2734			Gly-1 to Arg-8, Gly-17 to Val-25, Gln-27 to Gln-32, Ala-56 to Gly-64, Glu-121 to Thr-129, Arg-156 to Asp-174.	H0617: 2, L0758: 2, H0181: 1, L0521: 1, L0666: 1 and L0779: 1.		
HBGNJ14	914594	48	1 - 330	2735			Gly-3 to Thr-15, Pro-49 to Ser-54, Pro-56 to His-63, Gly-81 to Pro-87, Pro-92 to Thr-98.	H0617: 3		

HBGNM13	912730	49	12 - 197	2736			H0617: 2		
HBGNO07	952212	50	2 - 358	2737	Glu-14 to Cys-20, Glu-22 to His-32, Asp-39 to Thr-52, Lys-92 to Asp-101.		H0181: 1 and H0617: 1.		
HBGNQ31	887152	51	2 - 268	2738	Cys-7 to Gly-12, Ser-19 to Thr-26, Ala-31 to Leu-36, Ser-47 to Ser-57, Glu-75 to Phe-83.		AR054: 129, AR051: 118, AR050: 110 H0617: 4 and L0770: 2.		
HBGNW29	969396	52	24 - 263	2739	Gly-58 to Pro-69.		H0617: 2, H0663: 1 and H0181: 1.		
HBGOB07	883111	53	10 - 420	2740	Thr-21 to Lys-27, Cys-33 to Pro-38, Lys-68 to Trp-103, Pro-118 to Val-124, Pro-129 to Lys-137.		H0617: 2, L0439: 2, L0771: 1, L0766: 1, L0779: 1 and L0752: 1.		
HBGOJ28	967261	54	195 - 599	2741	Leu-30 to Thr-56, Arg-61 to Thr-71.		H0617: 2		
HBGOK53	848156	55	3 - 278	2742			H0617: 2		
HBGOL08	958290	56	1 - 369	2743			L0041: 2, H0617: 2, L0659: 1, L0438: 1 and L0601: 1.		
HBGPE04	926876	57	1 - 219	2744	Gly-22 to Ala-31, Arg-58 to Trp-73.		H0617: 2		
HBGPH02	918513	58	158 - 340	2745	Leu-14 to Pro-20, Ser-49 to Ile-55.		H0617: 2, L0780: 1, L0752: 1 and L0594: 1.		
HBGPK33	973425	59	14 - 274	2746			H0617: 4		
HBGPV05	930706	60	2 - 205	2747	Pro-13 to Arg-26.		H0617: 3		

HBGQG66	954302	61	1 - 309	2748	Met-3 to Asn-8, Ala-11 to Pro-39.	H0181: 1 and H0617: 1.		
HBGSD40	923142	62	3 - 413	2749	Arg-4 to His-10, Pro-14 to Thr-20, Glu-28 to Arg-35, Thr-40 to Ser-56, Thr-61 to Ser-75, Pro-93 to Arg-102, Asp-118 to Arg-124.	L0777: 3, H0617: 2, L0731: 2, H0606: 1, L0769: 1, L0803: 1, L0743: 1, L0744: 1, L0750: 1 and L0779: 1.		
HBGTK11	965509	63	1 - 273	2750	Pro-70 to Arg-78.	H0617: 3		
HBGTL01	914573	64	13 - 561	2751	Pro-28 to Trp-34.	L0794: 3, H0617: 2, L0750: 1 and L0758: 1.		
HBGTR84	886529	65	3 - 581	2752	Asp-43 to Arg-49, Glu-55 to Asp-64, Glu-75 to Arg-81, Leu-89 to Gly-98, Leu-110 to Lys-115, Asn-131 to Thr-141, Asn-152 to Lys-160.	AR051: 23, AR050: 17, AR054: 16 H0617: 4		
HBNAB01	966536	66	1 - 138	2753	Ser-8 to Leu-20.	H0253: 1 and H0188: 1.	17p13.1	191170, 191170
HBNAF14	660800	67	86 - 271	2754		H0618: 1 and H0188: 1.		
HBNAI71	655514	68	1 - 231	2755		H0188: 2		
HBNAN41	655842	69	123 - 302	2756	Asn-3 to Ser-15, Lys-21 to Asn-30.	H0188: 2		
HBNAW92	524954	70	2 - 226	2757	Gly-21 to Pro-27.	H0188: 2		
HBNAX71	530843	71	1 - 87	2758		H0188: 2		
HBNAY58	558193	72	245 - 400	2759	Leu-14 to Thr-20.	H0188: 2 and L0603: 1.		

HBNT52	524869	73	201 - 380	2760	Gln-48 to Pro-56.	H0188: 2	
HBZAJ09	655769	74	1 - 330	2761	Phe-13 to Phe-18, Gly-23 to Arg-38.	S0188: 2	
HBZSH16	655619	75	93 - 212	2762	Ser-1 to Ser-11.	S0190: 2	
HBZSH71	760418	76	116 - 301	2763	Thr-29 to Arg-34.	S0190: 2	
HBZSI73	655737	77	2 - 352	2764		S0190: 2	
HBZSK17	664013	78	111 - 383	2765	Val-3 to Lys-9.	H0059: 1 and S0190: 1.22q11.2-q13.2	123620, 138720, 145410, 188826, 231950, 239500, 275350, 600850
HCBMV01	914333	79	322 - 119	2766	Ser-1 to Met-6.	H0661: 1 and H0553: 1.	
HCBNW02	950897	80	183 - 521	2767		H0661: 2	
HCBNW07	951820	81	8 - 130	2768	Lys-28 to Phe-34.	L0770: 3, L0776: 3, H0686: 1, H0661: 1, L0021: 1, L0761: 1, L0766: 1, L0659: 1, L0647: 1, L0752: 1 and L0605: 1.	
HCBOG03	922351	82	2 - 283	2769	Lys-33 to Arg-38.	H0661: 2	
HCDMB01	915613	83	3 - 125	2770		S0398: 2	
HCDMB16	835781	84	2 - 181	2771		S0398: 2	
HCDMB60	726339	85	22 - 120	2772	Thr-6 to Leu-12, Tyr-19 to Lys-28.	S0398: 2	
HCDMC01	915239	86	2 - 901	2773	Ser-10 to Gly-23.	L0758: 13, H0253: 4,	

									H0618: 3, H0038: 1, L0779: 1 and S0398: 1.		
HCDMD23	676799	87	2 - 184	2774					S0398: 2		
HCHAD40	923764	88	78 - 269	2775	Lys-29 to Arg-34.				H0483: 2	13	
HCHAR16	675465	89	3 - 134	2776	Cys-1 to Pro-10, Thr-19 to Glu-28, Arg-36 to Asn-44.				H0483: 2		
HCHAR43	715128	90	1 - 366	2777	Ser-24 to Gly-29, Asn-47 to Pro-53, Pro-74 to Gly-79.				H0483: 2	Xp22.3	300077, 300500, 300650, 301200, 302350, 302950, 308700, 311200, 312040
HCHAR67	665184	91	1 - 318	2778	Phe-24 to Gln-30, Gln-32 to Leu-42.				H0483: 1 and H0550: 1.		
HCHBQ03	923763	92	190 - 459	2779	Asp-1 to Phe-21.				H0483: 4 and H0484: 1.	13	
HCHML32	668518	93	35 - 343	2780					H0484: 2		
HCHND96	880585	94	144 - 455	2781	Glu-14 to Ser-21, Asp-67 to Asp-73.				H0616: 7, L0758: 5, H0484: 1, H0040: 1, L0768: 1, L0774: 1 and L0775: 1.		
HCHOA76	740102	95	1 - 321	2782	Leu-26 to Cys-39, Cys-41 to Lys-50, Gly-87 to Glu-93.				H0484: 2		
HCHOD89	954866	96	2 - 214	2783	Glu-11 to Gly-17, Arg-25 to Ser-36.				H0484: 1 and H0483: 1.		

HCHPO55	717671	97	1 - 129	2784	Gly-1 to Gly-14.	H0484: 1 and H0483: 1.		
HCHQB06	934941	98	3 - 455	2785	Pro-13 to Gly-20, Ser-29 to Ala-45, Ser-66 to Ala-72, Phe-74 to Trp-87, Pro-102 to Arg-107.	H0484: 2, L0803: 1 and L0758: 1.		
HCMSE07	927904	99	522 - 896	2786	Ala-2 to Lys-10, Glu-70 to Gln-76.	AR089: 42, AR061: 34 H0651: 154, L0731: 9, L0777: 6, L0803: 4, L0775: 3, H0196: 2, H0163: 2, L0662: 2, L0805: 2, L0783: 2, L0438: 2, L0740: 2, L0759: 2, H0170: 1, S0444: 1, H0592: 1, H0632: 1, L0471: 1, H0399: 1, H0615: 1, H0040: 1, S0294: 1, H0647: 1, L0598: 1, L0763: 1, L0638: 1, L0637: 1, L0642: 1, L0374: 1, L0767: 1, L0768: 1, L0794: 1, L0804: 1, L0774: 1, L0375: 1, L0776: 1, L0606: 1, L0659: 1, L0809: 1, L0647: 1, L0789: 1, L0791: 1, L0666: 1, L0663: 1,		

								L0664: 1, L0665: 1, H0659: 1, H0658: 1, H0672: 1, S0328: 1, H0539: 1, S0380: 1, L0439: 1, L0779: 1, L0594: 1, L0361: 1, S0026: 1, S0242: 1 and S0460: 1.			
HCOMZ41	932878	100	120 - 296	2787	Arg-1 to Pro-10, Ile-21 to Gly-34.			L0768: 2, H0150: 1 and H0670: 1.			
HCOOG04	925748	101	68 - 3	2788	Tyr-10 to Cys-17.			H0670: 2			
HCOOI07	951665	102	75 - 458	2789	Ser-40 to Gly-45, Pro-55 to Asp-67.			H0670: 2			
HCOOM77	969161	103	83 - 283	2790				H0670: 2			
HCOOX10	961595	104	1 - 471	2791	Val-19 to Trp-24, Lys-70 to Lys-78, Ser-83 to Leu-100, Val-112 to Trp-117, Thr-119 to Lys-125, Cys-133 to Pro-143.			H0059: 1, L0803: 1 and H0670: 1.			
HCOOZ11	965306	105	89 - 592	2792	Asp-43 to Glu-48.			AR089: 15, AR061: 5 H0662: 2, H0670: 1, L0756: 1 and L0759: 1.	22q13.1-q13.2	103050, 103050, 124030, 124030, 138981, 182380, 188826, 190040, 190040, 190040	

HCOPP18	954332	106	259 - 585	2793	Gly-11 to Ser-16.	H0169: 2, L0809: 1, H0670: 1 and L0599: 1.		
HCOQE11	965299	107	409 - 684	2794	Gln-20 to Tyr-25, Asp-73 to Ser-79.	H0670: 4, L0776: 2, L0666: 2, L0759: 2, H0661: 1, L0717: 1, L0664: 1, L0779: 1, L0777: 1, L0752: 1 and L0755: 1.		
HCOQH12	969151	108	292 - 564	2795	Ala-52 to Lys-58, Gly-72 to Arg-79.	H0670: 2 and L0366: 1.		
HCOQQ07	951658	109	187 - 429	2796		H0670: 2		
HE8SG46	961388	110	1335 - 1553	2797	Glu-40 to Asn-46.	H0683: 122, L0740: 6, L0747: 5, L0438: 4, L0439: 4, L0756: 3, H0156: 2, L0521: 2, H0658: 2, L0754: 2, L0750: 2, L0779: 2, L0777: 2, L0731: 2, L0759: 2, H0171: 1, H0486: 1, H0244: 1, H0427: 1, H0310: 1, H0052: 1, H0263: 1, H0596: 1, L0163: 1, H0051: 1, H0328: 1, S0112: 1, L0768: 1, L0803: 1, L0774: 1, L0527: 1, L0517: 1, L0783: 1, L0666: 1, L0663: 1, H0670: 1, H0648: 1, S0152: 1,		



HEAAA42	963100	111	3 - 272	2798			S0146: 1, H0478: 1, L0752: 1, L0758: 1 and S0412: 1.		
							AR061: 8, AR089: 5 H0038: 4, H0616: 3, L0747: 3, L0663: 2, L0758: 2, H0369: 1, H0428: 1, L0769: 1, L0542: 1, L0809: 1, L0666: 1, L0665: 1, L0743: 1, L0777: 1, L0731: 1 and S0456: 1.		
HEAAB77	574510	112	1 - 360	2799		Glu-7 to Arg-24.	H0369: 2		
HEAAK46	574232	113	69 - 188	2800		His-33 to Val-39.	H0369: 2 and H0664: 1.		
HEAAM16	574008	114	114 - 221	2801			H0369: 2		
HEAAM52	960579	115	2 - 154	2802			H0369: 1 and H0040: 1.		
HEAAN18	932383	116	78 - 227	2803			H0369: 2		
HEAAQ66	653242	117	168 - 401	2804			H0369: 2		
HEAAT36	531348	118	114 - 488	2805		Phe-71 to Gln-78, Lys-87 to His-95.	L0748: 3, H0369: 1 and H0031: 1.		
HEAAT60	733632	119	121 - 471	2806		Gly-12 to Ile-18.	H0369: 2		
HEAAV10	968200	120	99 - 236	2807			H0369: 2		
HEAAV33	574508	121	219 - 449	2808		Asp-25 to Glu-30, Leu-39 to Val-48.	H0369: 2 and L0747: 1.		
HEDAE67	752875	122	1 - 147	2809		Ser-5 to Tyr-19, Arg-22 to Thr-32.	H0534: 4 and H0533: 3.		
HEEAD64	741305	123	1 - 159	2810		Glu-21 to Lys-30,	H0549: 2		

HEEAH07	851219	124	1 - 150	2811	Gly-33 to Ser-39.			
HEEAJ58	785121	125	246 - 1	2812	Pro-44 to Phe-50.	H0549: 2		
					Lys-25 to Gly-34,	H0549: 2		
					Pro-42 to Trp-57,			
					Lys-71 to Asp-82.			
HEEAJ76	887321	126	3 - 332	2813		AR054: 10, AR051: 9,		
						AR050: 8		
						H0549: 2		
HEEAK22	673904	127	140 - 253	2814	Gly-24 to Leu-30.	H0549: 2		
HEEAK84	780838	128	167 - 283	2815	Glu-12 to Gln-19.	H0549: 2		
HEEAL31	887312	129	3 - 203	2816	Val-19 to Ser-25,	H0369: 2 and H0549:		
					Arg-39 to Ser-60.	2.		
HEEAN24	676721	130	1 - 147	2817		H0549: 2		
HEEAS58	735620	131	3 - 278	2818	Ala-76 to Gly-84.	H0549: 2		
HEEAU79	706935	132	1 - 228	2819	Ala-17 to Gly-30,	H0549: 2 and L0600:		
					Arg-39 to Trp-46.	1.		
HEEAW01	851213	133	55 - 195	2820	Lys-12 to Trp-17.	H0549: 2		
HEEAW13	656299	134	28 - 168	2821	Phe-27 to Trp-32.	H0549: 2		
HEGAA24	676716	135	1 - 204	2822	Gly-1 to Glu-10,	H0550: 2		
					Gly-41 to Val-47.			
HEGAA73	767284	136	150 - 425	2823	Ser-52 to Trp-58.	H0550: 2		
HEGAB84	823900	137	1 - 351	2824	Ile-30 to Gly-36,	AR089: 13, AR061: 8		
					Thr-67 to Thr-72.	H0618: 2 and H0550:		
						1.		
HBGAC69	754344	138	281 - 475	2825	Ser-48 to Lys-54.	H0550: 2 and L0750:		
						1.		
HBGAC95	965183	139	113 - 355	2826		H0550: 1 and H0328:		
						1.		
HEGAI82	955291	140	1 - 330	2827	Ala-51 to Glu-60,	H0550: 1, H0644: 1		

HEGAK04	887299	141	54 - 305	2828	Pro-88 to Ser-104. Ala-29 to Lys-51, Arg-69 to His-75.	and L0659: 1. AR054: 16, AR051: 5, AR050: 3 H0550: 2 and L0749: 1.			
HEGAO83	780837	142	3 - 326	2829	Lys-1 to Ser-52.	AR089: 9, AR061: 7 H0550: 1 and H0253: 1.			
HEGAP06	934705	143	3 - 254	2830	Asn-4 to Asn-10, Gly-14 to Asp-21, Leu-26 to Gly-39.	L0754: 4, L0776: 2, L0743: 2, L0750: 2, L0779: 2, H0550: 1, L0769: 1 and H0658: 1.			
HEGAP31	697419	144	59 - 319	2831	Gly-1 to Gly-10, Glu-46 to Ser-52, Pro-61 to Pro-67, Arg-69 to Asp-75, Ser-82 to Ser-87.	H0550: 2			
HEGAP36	706951	145	117 - 239	2832	Tyr-36 to Thr-41.	H0550: 2			
HEGAR53	719387	146	462 - 644	2833	Val-1 to Leu-6, Arg-13 to Phe-18.	H0550: 1, H0212: 1, L0745: 1 and L0746: 1.			
HEGAY32	699906	147	1 - 195	2834	Leu-22 to Ser-28, Lys-36 to Lys-43, His-56 to Pro-65.	H0550: 2			
HEGAY52	726316	148	1 - 204	2835	His-32 to Trp-37, Pro-39 to Thr-53.	H0550: 2			
HEGAZ61	950033	149	12 - 560	2836	Leu-45 to Lys-50, Gln-55 to Glu-74, Thr-114 to Ile-119.	AR050: 66, AR054: 55, AR051: 37, AR089: 11, AR061: 6 H0549: 1 and H0550: 1.			

HEPAA44	509456	150	91 - 204	2837	Ala-6 to Gln-12.	H0150: 2			
HEPAB70	557149	151	90 - 353	2838	Ser-7 to Asp-20, Thr-30 to Phe-41, Gly-55 to Gly-61.	H0150: 2			
HEPAD09	888726	152	3 - 176	2839	Ala-20 to Gln-36, Pro-38 to Asn-50.	AR050: 154, AR051: 146, AR054: 141 H0150: 3	16q24.3	155555, 155555, 227650, 253000, 602783	
HEPAD40	509002	153	132 - 257	2840		H0150: 2			
HEPAD82	509452	154	3 - 113	2841	Ile-14 to Leu-22.	H0150: 3 and L0763: 1.			
HEPAJ70	586843	155	1 - 75	2842	His-1 to Thr-9.	H0150: 2	9q34.2-q34.3	120215, 120215, 190198	
HEPAK01	518331	156	73 - 309	2843	Asn-1 to Lys-7, Leu-27 to His-32, Arg-34 to Pro-50.	H0150: 2			
HEPAK41	925146	157	284 - 583	2844	Pro-4 to Arg-13, Val-34 to Asp-40.	H0549: 1, H0150: 1, L0761: 1 and L0764: 1.			
HEPAM29	508706	158	2 - 154	2845	Ser-9 to Leu-20, Thr-38 to Thr-44.	H0150: 2			
HEPAN19	508694	159	250 - 360	2846	Leu-13 to Lys-21.	L0758: 3, H0150: 2, L0803: 1 and L0779: 1.			
HEPAP02	926914	160	3 - 167	2847		H0150: 2	2p12	147200, 178640, 216900	
HEPAP12	968771	161	105 - 284	2848		H0150: 2			
HEPAS44	884083	162	3 - 260	2849		H0150: 2, L0369: 1			

HEPBA39	919875	163	3 - 518	2850	His-1 to Met-10.	and L0532: 1. AR061: 44, AR089: 13 H0150: 10, H0549: 5, H0176: 1, L0790: 1 and L0779: 1.		
HEPBB24	508684	164	42 - 179	2851		H0150: 3		
HEPBB60	855597	165	72 - 323	2852		H0150: 4		
HEPBG26	967921	166	4 - 204	2853		H0150: 2		
HEPBG35	508686	167	92 - 229	2854	Asp-15 to Gly-21, Gln-32 to Lys-45.	H0150: 2 and L0717: 1.		
HEPBH28	508673	168	171 - 290	2855	Glu-7 to Gln-12.	H0150: 2, L0809: 1, L0731: 1 and L0758: 1.		
HEPBH38	707524	169	99 - 257	2856		H0150: 2		
HEPBH45	508696	170	193 - 312	2857		H0150: 3		
HEPBO69	888697	171	112 - 216	2858		H0150: 5		
HEPBQ47	713836	172	91 - 291	2859	Pro-4 to Ser-12.	H0150: 2		
HEPBQ69	888693	173	272 - 460	2860	His-25 to Ile-31.	AR050: 7, AR054: 1 H0150: 3		
HEPBS10	968665	174	123 - 296	2861	Ala-1 to Asp-7.	H0150: 2		
HEPBX43	715685	175	2 - 445	2862	Pro-12 to Gly-22.	H0549: 2 and H0150: 2.		
HEPCD36	523670	176	37 - 297	2863	Asp-18 to Thr-28.	H0150: 2 and H0165: 1.		
HEPCE25	529343	177	2 - 121	2864		H0150: 2		
HEPCO59	761094	178	19 - 117	2865		H0150: 2		
HEPCT32	947081	179	227 - 685	2866	Ser-20 to Lys-30, Ala-43 to Ser-48, Ser-65 to Thr-72, Thr-112 to Thr-118,	AR051: 15, AR054: 2, AR050: 0 H0150: 4, H0038: 3, L0758: 3 and L0779: 2.		

HEPCU32	931824	180	448 - 975	2867	Ala-139 to Arg-147. Arg-57 to Arg-64, Arg-106 to Arg-116, Gln-128 to Pro-135.	AR051: 9, AR054: 8, AR050: 1, AR061: 0, AR089: 0 H0150: 2, H0270: 1, H0032: 1, H0212: 1 and L0779: 1.			
	946975	2652	345 - 872	5339	Arg-57 to Arg-64, Arg-106 to Arg-116, Gln-128 to Pro-135.				
	911438	181	2 - 160	2868	Pro-11 to Gly-16, Gln-37 to Gln-43.	AR089: 1, AR061: 0 H0544: 1 and H0435: 1.			
HEQAE65	699690	182	1 - 186	2869		H0544: 1 and H0038: 1.	5p13	108962, 120940, 217050, 217050, 217070, 245050, 600837, 600946, 600946, 600946	
HEQAO76	769973	183	86 - 436	2870	Ser-3 to Phe-65, Glu-78 to Ala-91, Ala-95 to Ser-116.	H0544: 2	7		
HEQAZ52	727051	184	10 - 180	2871		H0544: 2 and L0748: 2.			
HEQBA41	712243	185	80 - 529	2872	Pro-1 to Glu-15, Pro-29 to Val-35.	H0544: 1 and H0038: 1.			

HETAD29	509311	186	3 - 89	2873	Asn-13 to Cys-19.	H0046: 2	
HETAF20	509308	187	61 - 273	2874	Pro-22 to Gln-32.	H0046: 3	
HETAF49	509306	188	63 - 362	2875	Lys-1 to Val-24, Val-27 to Leu-32.	H0046: 2 and L0748: 2.	
HETAF89	509300	189	3 - 248	2876		H0046: 2	
HETAH16	942612	190	1 - 348	2877	Asn-1 to Gly-13, Val-23 to Ser-28, Ala-52 to Thr-63, Asp-75 to Thr-80.	H0046: 3	
HETAH66	799665	191	161 - 364	2878	Lys-14 to Pro-22.	H0046: 6	
HETAH67	535390	192	128 - 226	2879		H0046: 4	
HETAJ26	508994	193	3 - 164	2880	Ser-20 to Pro-25.	H0046: 2	
HETAK75	518156	194	3 - 290	2881		H0046: 2	
HETAN20	535359	195	2 - 202	2882		H0046: 4	
HETAP59	509118	196	162 - 305	2883	Gln-15 to Ser-21.	H0046: 3	
HETAP94	960392	197	17 - 136	2884	Pro-13 to Gln-22, Arg-24 to Cys-30, Thr-35 to Lys-40.	H0046: 5	
HETAR06	960839	198	2 - 313	2885	Ile-18 to Gln-23, Ser-36 to Ser-41.	H0046: 3	
HETAR60	934444	199	1 - 162	2886		H0046: 3	
HETAT83	918730	200	634 - 801	2887		H0046: 58 and H0616: 1.	
HETAZ13	536192	201	156 - 275	2888	Arg-35 to Glu-40.	H0046: 1 and S0004: 1.	
HETBA01	509189	202	33 - 203	2889		H0046: 2	
HETBF45	508655	203	1 - 138	2890		H0046: 2	
HETBH48	720853	204	81 - 257	2891	Asp-11 to Gln-18, Pro-38 to Ser-43.	H0046: 3	
HETBR25	509099	205	3 - 311	2892	Phe-1 to Ser-6,	H0046: 2 and L0741:	

						Arg-26 to Lys-31, Arg-54 to Ser-59.	1.			
HETBW39	523046	206	3 - 125	2893		Thr-3 to Thr-9, Ala-24 to Cys-29.	H0046: 2			
HETCE12	971505	207	354 - 647	2894			H0046: 5, L0748: 2 and L0527: 1.			
HETCE55	508666	208	143 - 307	2895		Gly-20 to Gly-27.	H0046: 3 and L0748: 1.			
HETCG63	841924	209	542 - 1249	2896		Asn-1 to Ile-20, Tyr-29 to Lys-41, Thr-68 to Gln-74, Asp-88 to Tyr-101, Lys-108 to Cys-116, Thr-136 to Thr-145, Thr-158 to Cys-171, Ser-183 to Pro-188.	H0046: 68, S0013: 2, H0369: 1, H0431: 1, H0013: 1, H0156: 1 and S0014: 1.			
HETCH92	921390	210	121 - 204	2897			H0046: 2			
HETCL55	522829	211	31 - 201	2898		Ala-32 to Pro-57.	H0046: 2			
HETDA81	525412	212	119 - 361	2899		Thr-56 to Pro-62, Asp-76 to Gly-81.	H0046: 2 and H0648: 1.			
HETDD18	509110	213	149 - 283	2900		His-3 to Asn-10.	H0046: 3			
HETDE67	883018	214	107 - 364	2901		Lys-25 to Asn-35.	H0046: 1 and H0615: 1.			
HETDE86	855509	215	54 - 398	2902		Tyr-1 to Ala-9.	H0046: 3 and L0617: 1.	22q11.2	123620, 138720, 145410, 231950, 239500, 275350, 600850	



HETDG67	960870	216	446 - 652	2903		H0046: 10 and S0152: 1.		
HETDI03	925489	217	1 - 159	2904	Asn-1 to Arg-14.	H0046: 2		
HETDL92	508990	218	146 - 274	2905		H0046: 2		
HETDN90	695021	219	131 - 235	2906	Leu-1 to Ser-6.	H0046: 2		
HETDP21	525407	220	116 - 295	2907		H0031: 2 and H0046: 1.		
HETDT15	660714	221	191 - 397	2908		H0046: 2 and L0756: 1.		
HETDW59	827093	222	180 - 281	2909		H0046: 2		
HETEB68	917400	223	39 - 248	2910	His-7 to Thr-22.	H0046: 9		
HETEQ16	952297	224	1 - 273	2911	Arg-1 to Ile-29.	H0046: 5		
HETEZ43	529591	225	189 - 359	2912	Asn-8 to Trp-15, Leu-20 to Ser-32.	H0046: 2	Xq26.1	300123, 301201, 301845, 301900, 304340, 307150, 307700, 308000, 308000, 309000, 310490, 313850
HETFA40	523112	226	195 - 476	2913	Asn-1 to Asp-10, Asp-25 to Gly-30, Asp-45 to Asp-56.	H0046: 3		
HETFC82	799658	227	1 - 543	2914		H0046: 5 and L0665: 1.		

HETFE48	974351	228	283 - 510	2915			H0046: 14		
HETFG29	795274	229	275 - 643	2916		Ala-22 to Tyr-27, Val-58 to Arg-75, Ala-82 to Gly-88, Pro-97 to Gln-102, Val-109 to Asp-117.	H0046: 3, H0618: 1, H0038: 1 and H0616: 1.		
HETFI24	954104	230	430 - 1149	2917		Arg-1 to Lys-6, Glu-8 to Ser-15, Leu-17 to Leu-24, Gln-26 to Gln-46, Ala-58 to Gln-63, Gln-68 to Leu-74, Lys-82 to Arg-95, Glu-101 to Pro-107, Leu-139 to Lys-147, Glu-176 to Leu-186, Arg-208 to Ile-215.	H0046: 53, H0616: 1 and L0664: 1.		
HETFI81	523398	231	66 - 239	2918			H0046: 2		
HETFL39	973697	232	208 - 405	2919		Gln-42 to Gly-48.	H0046: 2		
HETFM43	973702	233	88 - 339	2920		Lys-6 to His-12, Gly-20 to Gly-40, Gly-55 to Glu-69.	H0046: 9		
HETGH30	527929	234	2 - 127	2921		Asn-9 to Gly-17.	H0046: 2		
HETGI40	505383	235	1 - 63	2922		Gly-6 to Asn-21.	H0046: 2		
HETGL62	523372	236	2 - 154	2923			H0046: 2 and L0771: 1.		
HETGL74	947978	237	3 - 581	2924			AR050: 47, AR051: 46, AR054: 39, AR089: 4, AR061: 2 H0046: 4		

HETGN20	927789	238	7 - 567	2925		H0046: 2 and L0519: 2.		
HETGQ76	542486	239	23 - 190	2926	Pro-4 to Lys-11.	H0046: 2		
HETGS09	969632	240	11 - 109	2927		H0046: 2		
HETHD30	935175	241	151 - 441	2928	Arg-1 to Pro-7, Pro-13 to Ser-18, Ala-51 to Ser-64, Asn-92 to Lys-97.	H0046: 9		
HETHE56	974348	242	101 - 259	2929		H0046: 4		
HETHH49	967737	243	490 - 639	2930		H0046: 4		
HETHO63	745503	244	90 - 428	2931		H0046: 1, H0032: 1 and L0740: 1.		
HETHO78	963592	245	475 - 660	2932	Ser-12 to Val-20.	H0046: 5		
HETHR24	851412	246	24 - 461	2933	Pro-1 to Arg-7, Thr-18 to Thr-29, Arg-35 to Ser-50, His-87 to Cys-92.	AR089: 1, AR061: 0 H0046: 2		
HETHT53	974555	247	302 - 439	2934		H0046: 3		
HETTF01	966185	248	47 - 223	2935		H0046: 3		
HETIG71	974359	249	262 - 411	2936	Ser-3 to Pro-10.	H0046: 3		
HETIJ84	766589	250	1 - 363	2937	Ala-60 to Lys-67, Gln-71 to Gly-76.	H0046: 14		
HETIJ85	883991	251	1 - 135	2938	Glu-7 to Glu-12.	H0046: 2		
HETIQ89	764951	252	81 - 245	2939	Ile-3 to His-12.	H0046: 2		
HETIU60	739804	253	458 - 646	2940		H0046: 3		
HETIY84	935947	254	62 - 166	2941	Arg-16 to Asn-21.	H0046: 2		
HETJD30	974558	255	252 - 503	2942	Pro-49 to Thr-57.	H0046: 18		
HETJD86	909130	256	3 - 215	2943	Pro-14 to Pro-19, Cys-35 to Ser-40.	H0046: 5 and L0766: 1.		

HETJG63	950017	257	94 - 462	2944	Val-10 to Asp-15.	AR061: 4, AR089: 2 H0046: 2 and H0616: 1.		
HETJI32	806435	258	262 - 552	2945		L0375: 3, H0046: 2, L0774: 1 and L0789: 1.		
HETJK67	751072	259	173 - 433	2946	Ser-1 to Thr-7.	H0046: 2		
HETJN51	767932	260	26 - 274	2947		H0046: 2		
HETJT95	789310	261	222 - 413	2948	Lys-8 to Thr-23.	H0046: 3		
HETJX04	927120	262	3 - 704	2949	Asp-11 to Val-21, Pro-27 to Thr-43, Trp-92 to Lys-97, Pro-136 to Gly-149, Met-182 to Val-193, Thr-197 to Asn-203.	AR089: 4, AR061: 2 H0046: 1, H0032: 1, H0040: 1 and L0565: 1.		
HETJY11	966194	263	254 - 481	2950		H0046: 4 and L0774: 1.		
HETKA38	894600	264	3 - 308	2951	Val-50 to Arg-63, Asp-75 to Trp-89, Pro-92 to Arg-98.	H0046: 3 and H0616: 1.		
HETKG67	974355	265	321 - 527	2952		H0046: 11	17	
HETKH01	915320	266	20 - 226	2953		H0046: 3		
HETKH92	790910	267	1 - 210	2954	Pro-1 to Gly-14, Gly-17 to Ser-23, Ser-25 to Arg-34.	H0046: 2		
HETKM55	974362	268	31 - 267	2955	Ser-12 to Arg-18, Gln-69 to Met-74.	H0046: 17		
HETKQ65	855449	269	3 - 353	2956	Leu-33 to His-38, Pro-56 to Glu-61, Pro-111 to Leu-117.	H0046: 3		

HETKV26	910030	270	2 - 664	2957	Asp-12 to Trp-20.	AR061: 1, AR089: 0 H0046: 2		
HETKX91	789797	271	150 - 254	2958	Leu-22 to Arg-28.	H0046: 2		
HETKZ65	941045	272	3 - 620	2959	Gln-1 to Glu-20.	H0046: 2		
HETLB04	920894	273	518 - 1333	2960	Glu-1 to Gly-6, Val-21 to Asp-27.	H0046: 6 and H0616: 1.		
HETLH89	786458	274	2 - 250	2961	Cys-22 to Asp-27.	H0046: 2		
HETLM46	974361	275	111 - 314	2962	His-1 to Leu-8, Lys-10 to Leu-17, Met-44 to Cys-49.	H0046: 3		
HJMAE34	957079	276	3 - 305	2963		H0545: 2		
HJMAZ84	919847	277	39 - 335	2964		H0545: 2		
HJMBT23	858254	278	610 - 155	2965	Asp-53 to Gln-59, Asp-122 to Leu-128.	H0545: 2, L0766: 1, L0775: 1, L0383: 1, L0742: 1 and L0747: 1.		
HLMNG77	675752	279	103 - 252	2966	Arg-11 to Ser-19.	H0618: 6, L0758: 3, H0484: 1, H0255: 1, H0549: 1, H0253: 1, H0616: 1, L0794: 1, L0774: 1 and L0779: 1.		
HLWAB50	856552	280	167 - 367	2967	Tyr-23 to Ser-30.	H0553: 2		
HLWAD08	958554	281	146 - 295	2968	Asn-34 to Leu-40.	H0553: 2, L0441: 1 and H0672: 1.		
HLWAG51	964389	282	588 - 989	2969	Ser-84 to Ile-92, Glu-104 to Gly-111.	L0754: 20, L0748: 10, L0749: 10, H0553: 8, L0755: 8, H0031: 7, H0644: 6, H0030: 2, L0142: 1, L0771: 1, L0759: 1 and H0008: 1.		

HLWAH41	944774	283	13 - 771	2970	Arg-9 to Val-17, Pro-25 to Gly-30.	AR061: 2, AR089: 2 L0748: 6, L0752: 5, H0553: 2, L0754: 2, L0749: 1 and L0780: 1.		
	948953	2653	687 - 286	5340	Gly-1 to Ser-6, Phe-12 to Trp-25, Ala-31 to Gly-42, Met-44 to Gln-49.			
HLWAI13	920690	284	158 - 376	2971		L0754: 2, H0553: 1, H0670: 1 and L0749: 1.		
HLWAJ64	746460	285	381 - 145	2972		H0553: 2		
HLWAK69	694216	286	118 - 333	2973	Asn-12 to Ala-18, Gly-61 to Ser-70.	H0553: 1, H0435: 1 and L0748: 1.		
HLWAK94	715727	287	330 - 175	2974		H0553: 2, L0536: 2, L0754: 2 and H0030: 1.		
HLWAR77	947484	288	1287 - 292	2975	Gln-97 to Pro-114, Trp-117 to Lys-129, Thr-166 to Gln-173, Ser-178 to Lys-183, Glu-250 to Phe-256, Ser-295 to His-301, Tyr-307 to Gln-316, Glu-322 to Ser-330.	AR050: 21, AR054: 9, AR051: 3, AR089: 1, AR061: 1 H0553: 4 and L0759: 2.		
HLWAR78	723330	289	430 - 2	2976	Ser-20 to Gly-27, Gln-29 to Arg-41, Ser-46 to Pro-53.	H0553: 2, H0030: 1 and L0755: 1.		
HLWAU18	666273	290	4 - 390	2977	Arg-112 to Ser-117.	H0553: 2		
HLWBA11	966796	291	192 - 350	2978		H0553: 2		
HLWBA25	677944	292	1 - 192	2979	Lys-28 to Arg-39.	H0553: 2, L0005: 1, L0143: 1, L0749: 1 and		

HLWBE31	934562	293	1 - 150	2980	Val-2 to Pro-8, Arg-21 to Trp-29, Thr-41 to Arg-50.	L0755: 1. H0553: 2			
HLWBE92	791362	294	252 - 1	2981	Leu-6 to Gln-11, Arg-46 to Asp-52, Glu-68 to Pro-73.	H0030: 1 and H0553: 1.			
HLWBJ02	919639	295	90 - 380	2982	Ala-3 to Trp-10.	H0553: 2			
HLWBJ40	711000	296	78 - 224	2983		H0553: 3			
HLWBN49	713600	297	847 - 1062	2984	Arg-11 to His-20, Pro-23 to Gly-31.	L0748: 14, H0553: 4, L0754: 4, H0644: 3, H0031: 2, L0005: 1, L0774: 1, S0454: 1, L0749: 1 and L0780: 1.			
HLWBO68	529323	298	119 - 199	2985	Gly-1 to Glu-6, Val-8 to Tyr-16.	H0328: 2 and H0553: 1.			
HLWBQ84	782938	299	3 - 263	2986	Lys-1 to Lys-41, Pro-75 to Ser-86.	AR089: 1, AR061: 0 H0553: 2			
HLWBQ86	703465	300	109 - 279	2987	Met-36 to Lys-41.	H0553: 3			
HLWBS14	925300	301	272 - 48	2988	Ala-37 to Glu-48.	H0328: 1 and H0553: 1.			
HLWBS43	774175	302	2 - 268	2989	Glu-57 to Gly-66.	H0553: 2			
HLWBZ74	679215	303	184 - 2	2990	Asn-7 to Cys-15.	H0030: 1, H0553: 1 and L0754: 1.			
HLWCA67	577929	304	114 - 848	2991	Pro-26 to Ser-39, Ile-66 to Ser-78, Lys-84 to Pro-105, Pro-171 to Pro-181, Arg-194 to Ala-199.	H0031: 2, L0754: 2, H0553: 1, L0743: 1, L0748: 1 and L0747: 1.			

HLWCM44	727699	305	57 - 314	2992	Ala-17 to Thr-24.	H0553: 2		
HLWCM70	926850	306	207 - 329	2993		H0553: 2	3p24-p22	116806, 168468, 182280, 190182, 190182, 227646, 261510, 600163, 601154
HLWCO66	750779	307	71 - 208	2994	Gln-16 to Met-21, Val-25 to Lys-33, Ala-40 to Arg-46.	H0553: 2		
HLWCQ53	869700	308	160 - 348	2995	Ser-11 to Gly-17.	H0553: 2 and L0754: 1.		
HLWCQ62	742778	309	329 - 114	2996	Pro-10 to Lys-16.	H0615: 3, H0553: 2, L0756: 2 and L0758: 2.		
HLWCQ76	768018	310	2 - 154	2997		H0553: 2, L0656: 1, L0659: 1, L0666: 1, L0664: 1 and L0748: 1.		
HLWDA01	913768	311	2 - 463	2998	Ile-31 to Ser-40, Arg-115 to Gly-122.	H0553: 2		
HLWDB18	790969	312	1 - 702	2999	Ser-21 to Glu-27, Gln-50 to Pro-59, Gln-61 to Ser-66, Thr-68 to Pro-74, Pro-77 to Gln-84.	H0553: 2, H0038: 1, L0764: 1, L0794: 1 and L0438: 1.		
HLWDD02	953283	313	3 - 149	3000		H0553: 2		
HLWDE60	868276	314	148 - 426	3001	Tyr-8 to Arg-14, Asn-40 to His-46.	H0553: 2		



HLWDL71	759843	315	1 - 51 -		Val-56 to Thr-62.				
HLWEE76	973315	316	2 - 157	3002	Pro-1 to Gly-12.	H0553: 2			
HLWFG82	929647	317	1 - 558	3003	Thr-18 to Met-25.	H0553: 2			
				3004	Pro-4 to Pro-18, Gly-81 to Pro-87, Ala-110 to Ala-118, Gln-127 to Gly-143, Arg-168 to Asp-176.	AR054: 2, AR051: 1, AR089: 1, AR050: 1, AR061: 0 H0651: 59, L0751: 5, L0438: 4, L0774: 3, L0439: 3, L0748: 2, L0779: 2, L0752: 2, L0755: 2, L0595: 2, H0295: 1, H0009: 1, T0010: 1, H0553: 1, H0617: 1, H0163: 1, H0102: 1, H0494: 1, L0770: 1, L0662: 1, L0375: 1, L0806: 1, L0776: 1, L0657: 1, L0659: 1, L0792: 1, L0666: 1, L0663: 1, L0664: 1, L0665: 1, L0352: 1, H0648: 1, L0740: 1, L0749: 1, L0757: 1, L0361: 1, L0603: 1 and S0042: 1.			
HLWFQ04	856488	318	1 - 402	3005	Phe-20 to Gly-26, Ser-30 to Ser-37.	H0553: 2			
HMVDU41	957804	319	2 - 289	3006	Ser-37 to Ala-46, Cys-77 to Ser-85.	H0651: 29 and S0212: 1.			
HNBTP01	914428	320	3 - 512	3007		H0662: 2, H0670: 1, 22q13.1-q13.2	103050,		

								L0756: 1 and L0759: 1.		103050, 124030, 124030, 138981, 182380, 188826, 190040, 190040, 190040
HNBTT79	965424	321	3 - 194	3008	Pro-12 to Ser-24, Thr-42 to Ser-47, Pro-52 to Trp-59.			H0662: 2		
HNBTX52	965428	322	52 - 339	3009				H0662: 2		
HNBUM19	933672	323	209 - 472	3010				H0662: 2		
HNBUR07	951814	324	203 - 412	3011	Lys-8 to Asn-14, Lys-48 to Asp-53.			H0662: 2		
HNGAO08	958685	325	300 - 115	3012				H0651: 177, L0794: 5, L0766: 5, H0657: 3, L0526: 2, L0666: 2, L0664: 2, L0744: 2, L0759: 2, S0212: 1, S0360: 1, H0587: 1, H0052: 1, H0050: 1, H0266: 1, H0428: 1, H0551: 1, H0412: 1, L0475: 1, H0646: 1, L0761: 1, L0662: 1, L0803: 1, L0805: 1, L0809: 1, L0665: 1, S0052: 1, S0374: 1,		

								H0690: 1, H0659: 1, H0648: 1, H0521: 1, L0786: 1, L0779: 1, L0777: 1, L0780: 1, L0755: 1, H0543: 1 and S0424: 1.		
	959068	2654	81 - 284	5341	Ile-1 to Asp-7, Asn-39 to Pro-46.					
HNNNA06	917723	326	340 - 696	3013	Glu-15 to Asp-21, His-32 to His-45, Gly-55 to Lys-64, Gly-81 to Ser-88.			AR054: 7, AR050: 1, 2q35 AR051: 0 H0678: 47, L0748: 12, L0754: 7, L0747: 6, L0755: 5, L0776: 4, L0740: 4, L0749: 4, L0759: 3, H0553: 2, L0665: 2, L0779: 2, S0282: 1, H0057: 1, H0674: 1, H0616: 1, H0646: 1, L0770: 1, L0769: 1, L0646: 1, L0765: 1, L0773: 1, L0777: 1, L0731: 1 and L0596: 1.	118800, 123660, 125660, 125660, 193500, 193500, 193500, 193500, 201460, 205100, 237300, 262000, 600266, 601277	
HNNNA09	917724	327	320 - 520	3014	Glu-15 to Asp-21, His-32 to His-45.			H0678: 47, L0748: 12, L0754: 7, L0747: 6, L0755: 5, L0776: 4, L0740: 4, L0749: 4, L0759: 3, H0553: 2, L0665: 2, L0779: 2, S0282: 1, H0057: 1,	2q35	118800, 123660, 125660, 125660, 193500, 193500, 193500,

								H0674: 1, H0616: 1, H0646: 1, L0770: 1, L0769: 1, L0646: 1, L0765: 1, L0773: 1, L0777: 1, L0731: 1 and L0596: 1.		193500, 201460, 205100, 237300, 262000, 600266, 601277
HNNNA77	917725	328	771 - 1019	3015				H0678: 2	2q35	118800, 123660, 125660, 125660, 193500, 193500, 193500, 193500, 201460, 205100, 237300, 262000, 600266, 601277
HNOAS06	933730	329	525 - 752	3016	Asp-28 to Ala-37, Arg-49 to Gly-58, Ala-63 to Asn-69.			H0618: 3, L0758: 3, L0794: 2, L0748: 2, L0779: 2, L0755: 2, L0731: 2, L0770: 1, H0651: 1 and L0603: 1.		
HNOAX12	969363	330	231 - 524	3017	Pro-76 to Cys-88.			H0651: 8, L0744: 2, L0598: 1 and L0756: 1.		
HNOBF57	927903	331	101 - 475	3018	Ala-2 to Lys-10, Glu-70 to Gln-76.			H0651: 154, L0731: 9, L0777: 6, L0803: 4,		

							L0775: 3, H0196: 2, H0163: 2, L0662: 2, L0805: 2, L0783: 2, L0438: 2, L0740: 2, L0759: 2, H0170: 1, S0444: 1, H0592: 1, H0632: 1, L0471: 1, H0399: 1, H0615: 1, H0040: 1, S0294: 1, H0647: 1, L0598: 1, L0763: 1, L0638: 1, L0637: 1, L0642: 1, L0374: 1, L0767: 1, L0768: 1, L0794: 1, L0804: 1, L0774: 1, L0375: 1, L0776: 1, L0606: 1, L0659: 1, L0809: 1, L0647: 1, L0789: 1, L0791: 1, L0666: 1, L0663: 1, L0664: 1, L0665: 1, H0659: 1, H0658: 1, H0672: 1, S0328: 1, H0539: 1, S0380: 1, L0439: 1, L0779: 1, L0594: 1, L0361: 1, S0026: 1, S0242: 1 and S0460: 1.				
HNOCQ04	964933	332	3 - 374	3019			H0651: 6				
HNOCT39	952611	333	46 - 114	3020	Asn-18 to Lys-23.		H0651: 3				

HNOCU05	957833	334	536 - 745	3021		H0651: 2		
HOCMU03	922418	335	8 - 220	3022	Asp-9 to Lys-20, Ser-25 to Glu-30, Pro-57 to Asn-63.	H0660: 2		
HOCPIJ03	917484	336	3 - 185	3023		H0660: 2		
HODAD73	973463	337	91 - 231	3024	Gly-42 to His-47.	H0328: 3		
HODAD95	974043	338	280 - 426	3025		H0328: 2 and H0615: 2.		
HODAG37	529410	339	48 - 236	3026		H0328: 2		
HODAH32	859509	340	70 - 300	3027		H0328: 2 and L0534: 1.		
HODAJ01	921666	341	46 - 321	3028		H0328: 1 and H0615: 1.		
HODAJ35	529405	342	76 - 216	3029		H0328: 2		
HODAK38	529404	343	108 - 311	3030	Pro-10 to Cys-27, Gln-41 to Arg-48.	H0328: 2		
HODAK95	960179	344	147 - 398	3031		L0777: 4, H0328: 2, L0756: 2 and L0803: 1.		
HODAO16	529401	345	3 - 161	3032	Thr-3 to Lys-12.	H0328: 2		
HODAT56	529402	346	21 - 158	3033	Arg-15 to Thr-21, Ser-38 to Glu-44.	H0328: 2		
HODAV80	859519	347	85 - 300	3034		H0328: 2		
HODAW60	692684	348	227 - 328	3035		H0328: 2		
HODAW84	775425	349	142 - 297	3036	Thr-6 to Asp-14.	H0546: 1, H0328: 1, L0779: 1 and L0361: 1.		
HODBC01	921662	350	166 - 303	3037	Gly-2 to Arg-10, Ile-27 to Pro-33.	H0328: 3		
HODBC07	954161	351	158 - 331	3038	Arg-27 to Trp-33.	H0328: 2		
HODBE01	921655	352	18 - 116	3039	Cys-14 to Pro-20.	H0328: 2		

HODBH16	927781	353	3 - 299	3040	Glu-23 to His-30, Leu-41 to Asp-53.	H0328: 2	
HODBO85	859559	354	1 - 168	3041	Lys-13 to Gln-21.	H0328: 2	
HODBT58	678444	355	2 - 166	3042	Ser-39 to Arg-45.	H0328: 2	
HODBU95	529329	356	59 - 280	3043	Glu-10 to Ala-17.	H0328: 2	
HODBV71	761447	357	71 - 343	3044	Ser-22 to Val-41.	H0328: 1, H0059: 1 and L0596: 1.	
HODCA11	967732	358	1 - 180	3045		H0328: 2	
HODCA68	529400	359	2 - 184	3046	Leu-20 to Arg-25, Ser-47 to Gly-53.	H0328: 2	
HODCD05	932218	360	2 - 286	3047	Glu-35 to Ile-40, Pro-73 to Gln-79.	H0328: 1 and H0038: 1.	
HODCH64	529327	361	1 - 123	3048	Glu-1 to Thr-10.	H0328: 2	
HODCI11	967320	362	20 - 175	3049	Gln-44 to Thr-51.	H0328: 2	
HODCI42	932638	363	39 - 242	3050	Tyr-16 to Thr-22.	H0328: 2	
HODCL88	529334	364	1 - 222	3051		H0328: 2 and L0749: 2.	
HODCM62	859556	365	87 - 275	3052	Gln-1 to Ser-7, Arg-15 to Gly-21.	H0328: 2	
HODCO09	573202	366	1 - 168	3053	Lys-27 to Leu-32, Asp-49 to Asp-56.	H0328: 2	
HODCO46	573200	367	2 - 196	3054		H0328: 2	
HODCO82	573195	368	162 - 335	3055		H0328: 2	
HODCP69	507249	369	3 - 185	3056		H0328: 2	
HODCR43	529332	370	122 - 325	3057	Leu-1 to Lys-14.	H0328: 2	
HODCT07	954149	371	127 - 234	3058	Pro-14 to Ile-20, Pro-23 to Pro-28.	H0328: 2	
HODCU01	917270	372	15 - 203	3059	Arg-1 to Pro-12.	H0328: 2	
HODCU02	920698	373	313 - 477	3060	Gly-8 to Thr-22.	H0328: 1 and H0615:	

HODCU62	524314	374	207 - 323	3061	Arg-5 to Cys-11.	1.		
HODCV09	973487	375	382 - 591	3062	Lys-7 to Glu-12.	H0328: 2		
HODCW17	960051	376	156 - 284	3063	Lys-37 to Ser-43.	H0328: 3		
HODCW37	575256	377	80 - 280	3064	Pro-49 to His-59.	H0328: 2		
HODCZ20	859580	378	82 - 273	3065		H0328: 2		
HODDD20	933726	379	56 - 166	3066	Glu-21 to Glu-37.	H0328: 1 and H0615: 1.		
HODDD41	529390	380	3 - 305	3067	Ala-8 to Ala-13, Ile-17 to Gln-26, Phe-52 to Asn-64, Asp-72 to Lys-77.	H0328: 2		
HODDE28	529169	381	137 - 277	3068	Gln-14 to Leu-22, Lys-25 to Lys-35.	H0328: 2 and H0615: 1.		
HODDF51	937759	382	1 - 240	3069		H0328: 2		
HODDG57	806204	383	127 - 468	3070		H0328: 1, H0615: 1 and L0748: 1.		
HODDH52	742217	384	18 - 329	3071	Val-26 to Lys-38, Lys-47 to Lys-53, Lys-60 to Leu-65, Ser-80 to Ile-90.	H0038: 2, H0328: 1 and H0616: 1.		
HODDM21	523270	385	58 - 147	3072	Leu-16 to Arg-30.	H0328: 2		
HODDM25	780472	386	387 - 566	3073		H0328: 1, H0615: 1 and L0748: 1.		
HODDM78	859516	387	83 - 286	3074		H0328: 2		
HODDN40	859518	388	385 - 615	3075	Arg-10 to Arg-17, Ser-24 to Lys-30.	H0328: 1, H0615: 1 and L0758: 1.		
HODDN59	975437	389	391 - 660	3076		H0615: 2 and H0328: 1.		



HODDN93	891236	390	60 - 371	3077		AR054: 28, AR050: 22, AR051: 13 H0328: 1, H0674: 1 and L0754: 1.		
HODDQ02	920962	391	101 - 283	3078		H0328: 2		
HODDQ21	919295	392	3 - 359	3079	Tyr-11 to Gln-16, Ala-24 to Ala-32, Pro-36 to Ser-41.	H0615: 2 and H0328: 1.		
HODDR13	529640	393	48 - 152	3080		H0328: 2		
HODDS67	567197	394	171 - 338	3081		H0328: 2		
HODDU70	529290	395	1 - 357	3082	Gly-1 to Pro-7.	H0328: 2		
HODDX35	531209	396	126 - 275	3083	Leu-9 to Gln-20.	H0328: 2		
HODEA90	782242	397	391 - 534	3084		H0615: 3		
HODEB04	927022	398	1 - 282	3085		H0615: 3		
HODEC76	952204	399	350 - 514	3086		H0615: 2		
HODED11	966085	400	42 - 218	3087	Ile-12 to Thr-20, Tyr-47 to Gly-57.	H0615: 3		
HODED55	859368	401	24 - 296	3088	Thr-34 to Ser-40.	H0615: 2		
HODED87	915909	402	23 - 421	3089	Gln-3 to Arg-14, Pro-30 to Thr-36.	L0776: 2, L0740: 2, H0484: 1, H0615: 1, L0809: 1, L0748: 1, L0750: 1, L0779: 1 and L0752: 1.		
HODEF10	963494	403	235 - 480	3090		H0615: 2		
HODEF87	974342	404	27 - 266	3091		H0615: 3		
HODEG86	784833	405	373 - 648	3092		H0615: 3		
HODEH08	963895	406	2 - 142	3093	Pro-3 to Thr-10, Ser-38 to Pro-47.	H0615: 2		
HODEH22	974329	407	101 - 295	3094		H0615: 3		

HODEI13	859318	408	66 - 227	3095	Пе-9 to Cys-14, Pro-22 to Gly-27.	H0615: 3		
HODEI48	841906	409	511 - 633	3096	Lys-1 to Ser-10.	H0615: 3		
HODEK50	859307	410	363 - 740	3097	Ser-25 to Pro-30, Pro-84 to Glu-92.	H0615: 3		
HODEL92	859313	411	45 - 188	3098		H0615: 2		
HODEN75	772940	412	312 - 458	3099		H0615: 2		
HODEO87	930735	413	1 - 159	3100	Val-9 to Val-15.	H0615: 2		
HODEP04	926984	414	69 - 269	3101		H0615: 2		
HODEP12	965534	415	115 - 381	3102		H0615: 2		
HODEP86	784846	416	215 - 364	3103		H0615: 2		
HODEQ28	972808	417	206 - 331	3104	Thr-1 to Ser-13.	H0615: 3		
HODEQ79	859287	418	246 - 479	3105		H0615: 2		
HODER91	789661	419	1 - 351	3106	Phe-28 to Thr-33, Ile-44 to Thr-54, Arg-78 to Lys-88, Gln-99 to Lys-106.	AR061: 4, AR089: 2 H0651: 709, L0766: 5, L0754: 5, L0756: 3, L0803: 2, L0779: 2, L0777: 2, L0759: 2, S0354: 1, H0643: 1, H0013: 1, H0194: 1, H0545: 1, H0373: 1, H0252: 1, H0615: 1, H0316: 1, H0040: 1, H0641: 1, H0647: 1, S0422: 1, L0598: 1, L0369: 1, L0520: 1, L0762: 1, L0649: 1, L0804: 1, L0527: 1, L0656: 1, H0144: 1, H0702: 1, H0547: 1,		

HODES86	784815	420	3 - 278	3107			H0555: 1, H0436: 1, S0028: 1, L0746: 1, L0750: 1, L0780: 1, L0752: 1 and L0686: 1.		
HODET03	922988	421	27 - 191	3108		Val-36 to Gly-42.	L0753: 3, H0615: 1 and H0683: 1.		
HODEV13	859302	422	433 - 639	3109		Asn-37 to Lys-42.	H0615: 2		
HODEX10	926260	423	22 - 159	3110		Met-1 to Arg-6, Ser-16 to Lys-29.	AR061: 6, AR089: 3 H0615: 5		
HODEX31	922473	424	129 - 524	3111		Pro-19 to Gly-45.	H0615: 2		
HODEY08	972984	425	425 - 667	3112		Glu-1 to Lys-7, Thr-34 to Asn-43.	H0615: 2		
HODEY13	859323	426	179 - 382	3113			H0615: 2		
HODEY80	859296	427	432 - 677	3114		Gln-36 to Gly-41.	H0615: 2		
HODEZ02	918672	428	37 - 207	3115		Leu-27 to Ile-33, Trp-43 to Gln-48.	H0615: 2 and H0328: 1.		
HODEZ11	952166	429	178 - 336	3116			H0615: 2		
HODFA38	934266	430	170 - 397	3117		Ser-9 to Gly-15, Pro-22 to Lys-27, Glu-43 to Glu-56.	H0615: 3 and L0367: 1.		
HODFB05	929733	431	451 - 639	3118			H0615: 2		
HODFB57	972810	432	2 - 217	3119		Thr-1 to Ser-16.	H0615: 2		
HODFB88	792979	433	449 - 634	3120			H0615: 2		
HODFD08	958371	434	133 - 270	3121			H0615: 2		
HODFD10	963516	435	325 - 465	3122			H0615: 2		
HODFD45	780531	436	169 - 399	3123			H0615: 2		
HODFE69	859338	437	2 - 301	3124		Arg-46 to Ser-57, Thr-67 to Cys-78.	H0615: 2		

HODFG37	782219	438	263 - 433	3125			H0615: 2		
HODFH02	915257	439	33 - 164	3126	Gln-15 to Ser-23, Gly-30 to Lys-36.		H0615: 3		
HODFH76	783783	440	143 - 391	3127	Lys-32 to Ser-37.		H0615: 2		
HODFJ01	859549	441	247 - 501	3128			H0328: 1 and H0615: 1.		
HODFK18	974313	442	44 - 343	3129	Ala-14 to Ser-38.		H0615: 5 and L0665: 2.		
HODFK94	974318	443	42 - 182	3130	Ser-7 to Lys-15, Val-17 to Pro-29.		H0615: 3		
HODFL91	918456	444	1 - 159	3131	Pro-45 to Cys-51.		H0615: 2		
HODFN19	859334	445	198 - 425	3132			H0615: 2		
HODFN42	921529	446	79 - 318	3133			H0328: 1 and H0615: 1.		
HODFO03	859329	447	124 - 309	3134	Asp-1 to Asp-7.		H0615: 3 and H0328: 2.		
HODFO37	859314	448	85 - 306	3135	Trp-44 to Thr-54.		H0615: 2		
HODFP40	921651	449	587 - 817	3136	Tyr-4 to Thr-11, Thr-15 to Asp-20, Arg-29 to Leu-42.		H0328: 1, H0615: 1, L0775: 1, H0648: 1 and L0758: 1.		
HODFQ02	918637	450	427 - 615	3137	Tyr-1 to Cys-14, Gln-20 to Ile-47.		H0615: 3		
HODFQ06	934304	451	258 - 401	3138	Thr-1 to Asn-6.		H0615: 2		
HODFT52	915232	452	224 - 51	3139			H0615: 2		
HODFU02	918536	453	204 - 398	3140			H0615: 2		
HODFU06	934229	454	460 - 588	3141	Thr-1 to Ser-6.		H0615: 3		
HODFU47	806232	455	274 - 582	3142	Glu-1 to His-6, Phe-13 to Pro-23, Arg-29 to Leu-34.		H0615: 2 and L0558: 1.		

								Pro-54 to Asp-60, Pro-62 to Gly-67.			
HODFU54	965526	456	60 - 134	3143						H0615: 2	
HODFW17	859322	457	370 - 603	3144						H0615: 2	
HODFX57	975259	458	1 - 183	3145						H0615: 3	
HODFY16	958329	459	163 - 309	3146						AR061: 6, AR089: 3 H0615: 2 and L0766: 1.	
HODFY79	975253	460	393 - 259	3147						H0615: 3	
HODFZ11	965104	461	45 - 209	3148						H0615: 2 and H0169: 1.	
HODGC04	926863	462	83 - 214	3149				Glu-9 to Gln-21.		H0615: 2	
HODGC61	973449	463	43 - 324	3150				Thr-50 to Gln-57.		AR061: 8, AR089: 5 H0615: 3	
HODGD05	931071	464	1 - 147	3151				Ala-8 to Gln-29, Ser-36 to Gly-44.		H0615: 2	
HODGH02	917969	465	28 - 285	3152				His-8 to Gly-18, Leu-37 to Lys-42.		H0615: 2	
HODGH04	926255	466	10 - 159	3153				His-8 to Gly-18, Gly-26 to Arg-33.		H0615: 2	
HODGH07	951933	467	178 - 330	3154						H0615: 2	
HODGH11	965105	468	383 - 556	3155						H0615: 2	
HODGH91	968794	469	91 - 333	3156				Arg-30 to Asn-35. 1.		H0328: 1 and H0615: 1.	
HODGI08	958235	470	1 - 267	3157				Arg-11 to Thr-29.		H0615: 2	
HODGJ67	974297	471	3 - 353	3158				Ser-2 to Thr-13, Ile-16 to Ser-26, Pro-28 to Gln-36, Gln-41 to Pro-47.		H0615: 3	

HODGL54	859303	472	402 - 698	3159	Pro-25 to Ser-31.	H0615: 4 and H0328: 1.		
HODGM46	974051	473	2 - 304	3160	Phe-81 to Phe-87.	H0615: 3		
HODGO46	883087	474	292 - 525	3161		H0615: 2		
HODGP37	974293	475	67 - 228	3162		H0615: 3		
HODGP83	889967	476	3 - 236	3163		H0615: 2		
HODGP95	908650	477	23 - 358	3164	Lys-38 to Arg-44, Thr-84 to Asp-99.	AR089: 8, AR061: 3 H0615: 2		
HODGQ08	958237	478	261 - 377	3165		H0615: 2		
HODGQ22	974290	479	117 - 245	3166		H0615: 3		
HODGQ32	974294	480	175 - 405	3167	Val-1 to Lys-7, Gln-12 to Arg-18, Arg-22 to Gln-30, Gly-32 to Glu-40.	H0615: 3		
HODGQ92	894368	481	2 - 274	3168	Asp-42 to Arg-47, Gln-84 to Gly-91.	AR061: 5, AR089: 2 H0615: 2		
HODGT62	974052	482	253 - 402	3169		H0615: 3		
HODGW08	958277	483	183 - 371	3170	Ala-11 to Cys-16.	H0615: 2		
HODGX10	963427	484	206 - 310	3171		H0615: 3		
HODGX29	913879	485	138 - 257	3172		H0615: 2 and H0658: 1.		
HODGZ06	933783	486	315 - 479	3173		H0615: 2		
HODGZ10	961977	487	3 - 119	3174		H0615: 2		
HODHC03	922987	488	3 - 341	3175	Pro-59 to Pro-65, Glu-96 to Phe-113.	H0615: 2 and L0777: 1.		
HODHD16	974924	489	132 - 278	3176	Ala-1 to Glu-12.	H0615: 3 and H0328: 1.		
HODHG71	926203	490	190 - 384	3177	Asp-1 to Lys-20, Cys-34 to Ser-42.	H0615: 2		

HODHH82	964935	491	78 - 293	3178	Thr-14 to Arg-22, Ile-25 to Ser-35.	H0328: 1 and H0615: 1.		
HODHI07	952195	492	376 - 636	3179	Glu-33 to Lys-46.	H0328: 1 and H0615: 1.		
HODHI26	973423	493	275 - 451	3180		H0615: 2 and H0328: 1.		
HODHK02	918613	494	108 - 302	3181		H0615: 3		
HODHL19	973433	495	79 - 315	3182		H0615: 3		
HODHL56	847724	496	185 - 415	3183		H0615: 2, H0188: 1 and L0758: 1.		
HODHO11	965529	497	36 - 137	3184		H0615: 2		
HODHS34	965460	498	285 - 461	3185		H0615: 2		
HODHY53	914554	499	47 - 214	3186		H0615: 2		
HODJR03	922484	500	134 - 379	3187		H0615: 3		
HODJY33	951404	501	31 - 384	3188	Lys-30 to Arg-36.	H0615: 3		
HODJZ90	965049	502	41 - 169	3189	Lys-8 to Ser-14.	H0615: 2		
HODKN07	933320	503	92 - 256	3190	His-20 to Val-35.	H0615: 2 and L0060: 1.		
HOFAA15	659522	504	71 - 385	3191	Ile-13 to Arg-20.	H0415: 1 and H0414: 1.		
HOFAB40	964113	505	527 - 99	3192		H0415: 2 and H0414: 1.		
HOFAB71	573337	506	100 - 249	3193		H0414: 2		
HOFAD05	932211	507	118 - 306	3194	Pro-1 to Arg-8, Pro-39 to Glu-56.	H0415: 1 and H0414: 1.		
HOFAE31	772992	508	2 - 220	3195	Glu-1 to Leu-8, Arg-38 to Cys-49.	H0414: 2		
HOFAE61	707359	509	3 - 293	3196	Val-18 to Arg-31, Arg-36 to Pro-42.	H0415: 1 and H0414: 1.		

HOFAF84	868887	510	136 - 273	3197	Arg-57 to Cys-62.				
HOFMA24	782275	511	63 - 347	3198	Gly-30 to Gly-46.		H0414: 2		
HOFMB78	572941	512	1 - 399	3199	Ser-2 to Arg-15.		H0415: 2		
					Arg-10 to Lys-23.		AR089: 26, AR061: 10		
							H0415: 8 and H0414: 2.		
HOFMB83	572839	513	3 - 158	3200	Thr-7 to Gly-18,		H0415: 2		
					Pro-20 to Gly-26.				
HOFMD13	916959	514	232 - 405	3201			H0415: 2		
HOFME41	867993	515	55 - 264	3202			H0415: 2		
HOFMF03	924679	516	3 - 446	3203	Lys-36 to Ala-52,		H0415: 2		
					Thr-54 to His-61,				
					Pro-90 to Thr-96.				
HOFMF70	734917	517	1 - 387	3204	Pro-31 to Arg-36,		H0415: 2	13q11-q12	121011, 121011, 129500, 253700, 601885, 602221
					Glu-41 to Gln-52.				106150, 106150, 145260, 173870, 173870, 600759, 600996, 601744, 601975
HOFMG21	973358	518	66 - 497	3205	Pro-1 to Pro-6,		AR089: 6, AR061: 3	1q42	
					Asp-41 to Arg-67,		H0415: 3		
					Gly-100 to Val-106.				
HOFMH12	964722	519	2 - 478	3206	Arg-1 to Cys-16,		H0415: 3 and H0414: 1.		
					Tyr-59 to Lys-68,				



HOFMH38	920365	520	3 - 413	3207	Glu-76 to Arg-82. Ser-85 to Gly-100, Pro-102 to Ser-113.	AR089: 5, AR061: 3 H0415: 1 and H0414: 1.	5	
HOFMH95	973359	521	2 - 211	3208	Val-15 to Ala-22, Val-26 to Gly-38, Gln-65 to Gly-70.	H0415: 3		
HOFMI01	609722	522	2 - 121	3209	Cys-2 to Gly-7, Ala-14 to Pro-20.	H0415: 2		
HOFMI62	796358	523	3 - 452	3210	Asp-1 to Gly-22, Pro-24 to Gly-34.	H0415: 8 and H0414: 2.		
HOFMI63	745133	524	1 - 225	3211	Ala-4 to Gly-11, Pro-26 to Trp-31.	H0415: 2		
HOFMI44	719663	525	2 - 301	3212	Arg-1 to Asp-7, Ser-26 to Leu-39.	AR089: 30, AR061: 10 H0415: 1 and H0414: 1.		
HOFMK22	675122	526	3 - 359	3213	Asp-22 to Val-42, Phe-50 to Tyr-55, Leu-65 to Gln-70.	H0415: 2		
HOFMM27	973349	527	1 - 132	3214	Ala-5 to Trp-19.	H0415: 5 and H0414: 1.		
HOFMM72	464015	528	49 - 366	3215		H0415: 2		
HOFMN30	514556	529	422 - 234	3216		H0415: 2		
HOFMP31	698097	530	2 - 202	3217	Gly-1 to Pro-6, Pro-23 to Asp-28, Pro-36 to Ser-46, Lys-54 to Asn-63.	H0415: 2		
HOFMP79	775242	531	2 - 445	3218	Gly-1 to His-12, Ser-40 to Pro-66,	AR089: 11, AR061: 3 H0415: 2		

							Glu-79 to Lys-89, Glu-96 to Leu-105.				
HOFMQ04	823439	532	34 - 318	3219			Gly-11 to Leu-19, Val-23 to Gly-32, His-34 to Ser-45.			H0415: 1 and H0414: 1.	
HOFMQ31	906933	533	183 - 449	3220						H0415: 4	
HOFMQ65	789347	534	2 - 280	3221			Gly-1 to Ser-13, Arg-26 to Glu-35, Gly-38 to Met-48.			H0415: 2	
HOFMS68	464075	535	187 - 348	3222						H0415: 2	
HOFMS74	514568	536	340 - 2	3223			Thr-4 to Gly-9, Leu-32 to Glu-42, Pro-54 to Cys-68, Ile-97 to Gly-113.			H0415: 1 and H0435: 1.	
HOFMS89	575820	537	2 - 502	3224			Arg-34 to Thr-44, Pro-65 to Gly-79, Leu-98 to Ser-105.			H0415: 2	
HOFMT20	669738	538	2 - 157	3225			Asn-20 to Cys-29, Val-33 to Ser-40.			H0415: 2	
HOFMT43	811542	539	1 - 411	3226			Val-6 to Arg-12, Pro-19 to Thr-36, Ser-49 to Thr-54, Glu-61 to Trp-67, Pro-77 to Ala-84, Ser-104 to Asn-114.			H0415: 2	
HOFMT66	754251	540	2 - 169	3227			Arg-1 to Asn-8, Lys-20 to Gly-38.			H0415: 2	
HOFMT72	563575	541	3 - 248	3228			Gly-2 to Gly-9.			H0415: 1 and H0414: 1.	
HOFMU33	702492	542	2 - 373	3229			Arg-1 to Gly-20,			H0415: 2	

HOFMU63	744325	543	1 - 243	3230	Pro-45 to Ser-50.			
HOFMU75	713809	544	2 - 121	3231	His-8 to Trp-19.	H0415: 2		
HOFMV84	859109	545	3 - 230	3232	Lys-10 to Trp-15, Pro-47 to Ser-55, Pro-67 to Phe-76.	H0415: 2		
HOFNA04	615287	546	209 - 373	3233	Glu-19 to Gln-24, Thr-30 to Lys-38.	H0415: 2		
HOFNA92	792734	547	95 - 343	3234	Arg-1 to Gly-12.	H0415: 2		
HOFNC63	973354	548	203 - 3	3235	Tyr-1 to Pro-12.	H0415: 2		
HOFND14	658476	549	3 - 122	3236		H0415: 2		
HOFND40	867984	550	54 - 341	3237	Pro-80 to Trp-88.	H0415: 2		
HOFND50	727285	551	446 - 90	3238		H0415: 2		
HOFND52	727173	552	407 - 174	3239		AR054: 11, AR051: 3, AR050: 2 H0415: 2		
	888450	2655	2 - 325	5342	Ala-5 to Ala-13, Pro-15 to Lys-23, Ala-39 to Cys-44, Pro-47 to Cys-74, Ala-83 to Gly-90.			
HOFND90	716670	553	2 - 388	3240	Gly-1 to Asn-10, Gln-30 to Asp-35, Gln-44 to Gly-54, Ser-61 to Val-89, Ser-92 to Ser-98.	H0415: 2		
HOFND94	717067	554	67 - 225	3241	Thr-30 to Tyr-39.	H0415: 2		
HOFNG01	859106	555	140 - 280	3242	Gly-19 to Asn-24.	H0415: 2		
HOFNG06	935569	556	1 - 207	3243	Thr-18 to Trp-23.	H0415: 2		

HOFNH33	715101	557	3 - 152	3244	Asp-14 to Gly-20, Arg-45 to Ala-50.	H0415: 2		
HOFNI08	974435	558	1 - 426	3245		H0415: 4		
HOFNI48	708727	559	140 - 376	3246	Pro-2 to Gly-13, Gly-59 to Ser-64.	H0415: 2		
HOFNI82	717355	560	117 - 362	3247	Gly-36 to Tyr-50.	H0415: 3		
HOFN118	666498	561	1 - 405	3248	Ser-26 to Pro-33.	AR089: 9, AR061: 3 H0415: 1 and H0414: 1.		
HOFNL25	916963	562	41 - 346	3249	Lys-54 to Ser-60, Tyr-86 to His-93.	AR089: 8, AR061: 7 H0415: 3		
HOFNL37	906250	563	2 - 394	3250	Gly-1 to Pro-6, Thr-24 to Ala-30, Ser-33 to Pro-41, Ser-51 to Ser-61.	H0415: 6, H0414: 2, H0046: 1 and H0271: 1.	10p13	601362
HOFNL40	711205	564	1 - 225	3251		H0415: 2		
HOFNL92	770088	565	244 - 414	3252	Gln-1 to Pro-8.	H0415: 2		
HOFNM85	869113	566	2 - 340	3253		H0415: 2		
HOFNT59	615305	567	109 - 405	3254	Pro-7 to Ser-12, Glu-37 to Ser-42, Leu-45 to Gly-53, Leu-68 to Val-75, Ser-81 to Thr-86.	H0415: 2		
HOFNU72	705435	568	1 - 216	3255		H0415: 2	11p15.5	125852, 126452, 126452, 141900, 141900, 141900, 141900,

								141900, 141900, 142000, 142000, 142200, 142250, 142270, 176730, 176730, 176730, 190020, 191290, 192500, 192500, 194071, 194071, 204500, 600856, 601680, 602631, 602631
HOFNW10	916588	569	28 - 237	3256	Lys-1 to Ser-14.	H0415: 2		
HOFNW79	973351	570	6 - 365	3257		H0415: 8 and H0414: 2.		
HOFNY02	920218	571	217 - 495	3258		H0415: 2		
HOFNY50	715312	572	68 - 430	3259	Pro-15 to Pro-25, Lys-68 to Glu-76, Lys-89 to Arg-107.	H0415: 2		
HOFNZ15	660317	573	98 - 379	3260	Ser-18 to Ser-34.	H0415: 2		
HOFNZ16	859104	574	2 - 268	3261	Gly-1 to Pro-6.	H0415: 2		

HOFNZ21	677372	575	109 - 456	3262	Arg-1 to Gly-6.	H0415: 2	9p13-p12	230400, 250250
HOFNZ58	683473	576	29 - 229	3263		H0415: 2		
HOFNZ94	794308	577	99 - 218	3264		H0415: 1 and H0414: 1.		
HOFQA17	935553	578	142 - 369	3265	Gly-34 to Glu-39.	H0415: 2		
HOFQB88	751692	579	1 - 501	3266	Thr-2 to Val-11, Leu-18 to Gly-25, Pro-30 to Ser-35, Ala-40 to Pro-47, Lys-62 to Glu-70, Lys-76 to Arg-82.	H0415: 2		
HOFQB91	827631	580	1 - 234	3267		H0415: 2		
HOFQE94	924473	581	173 - 382	3268	Thr-1 to Ser-11, Ser-23 to His-29, Gly-53 to Gln-67.	H0415: 2		
HOFQF57	666909	582	3 - 419	3269		H0415: 2		
HOFQF84	739399	583	78 - 431	3270	Asn-1 to Gln-9, Pro-17 to Ala-30.	H0415: 2		
HOGAF39	947431	584	3 - 269	3271	Asp-1 to Leu-22, Val-26 to Trp-38.	H0435: 1 and S0152: 1.		
HOGAU90	954011	585	247 - 402	3272	Cys-10 to Asp-19.	H0615: 1 and H0435: 1.		
HOGAV36	926098	586	211 - 576	3273	Pro-8 to Lys-15, Arg-67 to Arg-74, Arg-76 to Gly-85, Glu-91 to Gly-97, Thr-113 to Phe-120.	H0663: 2, L0761: 1, L0771: 1 and H0435: 1.		
HOGBF78	575929	587	264 - 443	3274	Lys-1 to Val-7.	H0435: 2 and L0592:		

HOGCQ05	950216	588	381 - 193	3275	Pro-12 to Ala-17, Val-29 to Gly-36.	1. H0165: 1, H0435: 1 and L0747: 1.		
HOGCR32	575931	589	3 - 137	3276	Pro-3 to Lys-13, Thr-39 to Ile-45.	H0435: 2		
HOGCT45	717068	590	2 - 364	3277	Arg-1 to Glu-14, Thr-39 to Gln-45, Pro-52 to Lys-62, Glu-89 to Thr-94.	H0040: 1 and H0435: 1.		
HOGCX95	890607	591	52 - 660	3278		H0038: 2, L0758: 2, H0253: 1, H0616: 1, H0435: 1 and L0777: 1.		
HOGEE76	968956	592	732 - 298	3279		H0435: 2		
HOGEU49	961587	593	1 - 285	3280	Asp-25 to Ser-34, Tyr-39 to Gln-44, Leu-84 to Lys-90.	H0435: 1 and H0670: 1.		
HOOJQ59	965013	594	418 - 621	3281		H0648: 2, L0367: 1, H0651: 1, L0748: 1 and L0754: 1.		
HOVAF17	576627	595	215 - 358	3282		H0428: 2		
HOVAF71	757294	596	55 - 183	3283		H0428: 2		
HOVAG49	927320	597	2 - 298	3284		H0428: 2 and L0588: 1.		
HOVAI41	670963	598	3 - 107	3285		H0428: 2		
HOVAM50	723671	599	64 - 243	3286	Ser-22 to Arg-35, Lys-39 to Gly-44.	H0428: 2		
HOVAO76	770066	600	89 - 238	3287	Arg-15 to Gln-21.	L0754: 2, H0428: 1 and H0616: 1.		
HOVBQ10	964671	601	515 - 763	3288	Lys-21 to Gly-26.	L0777: 6, L0758: 5,		

								L0747: 2, H0428: 1, L0770: 1, L0768: 1, L0533: 1, H0666: 1, L0750: 1 and L0755: 1.			
HOVBY34	706816	602	2 - 295	3289			Gly-1 to Ala-8, Glu-67 to His-74.	H0428: 2			
HOVBZ26	888442	603	3 - 215	3290			Gly-37 to Arg-46, Ser-57 to Trp-70.	AR051: 44, AR050: 43, AR054: 30 H0428: 2			
HOVCA52	727170	604	232 - 354	3291				H0428: 2			
HOVCD39	705406	605	25 - 192	3292			Ser-8 to Leu-16.	H0428: 2			
HOVCI76	858845	606	60 - 284	3293			Arg-13 to Gly-18, Gln-44 to Ser-50.	H0428: 3			
HOVCI77	713792	607	119 - 241	3294			Lys-7 to Ser-16.	H0428: 2			
HOVCJ24	858844	608	68 - 319	3295			Leu-16 to His-22, Cys-50 to Pro-55.	H0428: 2			
HOVCM22	674177	609	219 - 482	3296			Ser-1 to Lys-14, Gln-48 to Asn-63, Glu-70 to Pro-88.	H0674: 2, H0549: 1 and H0428: 1.			
HOVCO11	970814	610	157 - 423	3297			Val-11 to Leu-18.	H0428: 2 and L0770: 1.	7p15	138079, 138079, 139191, 142959, 153880, 180104, 600994, 601649	
HOVCO58	736065	611	283 - 420	3298				H0428: 2			
HOVCQ47	496190	612	1 - 213	3299				L0758: 3, H0428: 2, L0794: 2, L0764: 1,			



HOVDY04	926219	613	81 - 320	3300	Ser-25 to Gly-45.	L0803: 1 and L0593: 1. L0769: 4, L0758: 3, L0717: 2, H0428: 2, L0794: 2, L0731: 2, L0591: 2, L0776: 1, L0786: 1 and L0779: 1.		
HOVEE58	968699	614	131 - 3	3301	Thr-11 to Pro-21.	H0428: 1 and H0032: 1.		
HOVEK70	909138	615	3 - 395	3302	Met-10 to Gly-18.	AR089: 10, AR061: 4 H0038: 4, H0616: 3, L0747: 3, L0758: 3, L0663: 2, H0369: 1, H0428: 1, L0769: 1, L0542: 1, L0809: 1, L0666: 1, L0665: 1, L0743: 1, L0777: 1, L0731: 1 and S0456: 1.		
HOVEV36	959234	616	128 - 307	3303		H0428: 2 and H0546: 1.		
HOVJA10	961467	617	37 - 225	3304		H0688: 3		
HPCAB21	573829	618	57 - 155	3305		S0146: 2		
HPCAB31	698320	619	96 - 230	3306		H0658: 1, S0146: 1 and L0754: 1.		
HPCAE18	574952	620	2 - 355	3307		S0146: 2	12q24	113100, 124200, 147440, 158590, 160781, 163950, 163950,

										251170, 276710, 600175, 601517
HPCAH18	573395	621	192 - 314	3308					S0146: 2	
HPCAH88	953808	622	488 - 637	3309					S0146: 2, H0046: 1, S0148: 1, L0439: 1 and L0745: 1.	
HPCAI21	655535	623	134 - 259	3310					S0146: 2	
HPCAI68	655536	624	58 - 168	3311			Lys-1 to Gln-6, Met-15 to Thr-29.		S0146: 2	
HPCAK16	662121	625	455 - 634	3312					H0615: 1, H0658: 1 and S0146: 1.	
HPCAK57	734931	626	265 - 420	3313					H0031: 1 and S0146: 1.	
HPCAL60	655723	627	41 - 142	3314			Gly-24 to Ser-34.		S0146: 2	
HPCAL86	924709	628	1 - 117	3315			Asn-12 to Ile-18.		S0146: 2.	
HPCAM22	655607	629	64 - 237	3316			Asp-26 to Phe-39.		S0146: 2	
HPCAN59	655742	630	91 - 210	3317					S0146: 2	
HPCAO04	655732	631	181 - 315	3318					S0146: 2	
HPCPF05	927168	632	88 - 249	3319					H0659: 2	
HPCPO07	951826	633	3 - 128	3320			Gly-29 to Tyr-34.		H0659: 2	
HPCQY57	927135	634	3 - 371	3321			Ser-34 to Gly-43, Lys-55 to Leu-71.		H0606: 1, L0803: 1 and H0659: 1.	
HPDOT03	922481	635	1 - 384	3322					H0549: 1, L0773: 1, L0768: 1, L0794: 1, L0803: 1, H0658: 1 and L0747: 1.	
HPDOY06	929318	636	22 - 201	3323					H0658: 2	
HPDPI69	966158	637	92 - 436	3324			Arg-7 to Tyr-14.		H0046: 17, H0658: 1	

HPDPK12	969340	638	155 - 316	3325			and H0672: 1.		
HPDPQ40	922464	639	2 - 223	3326	Ile-10 to Asn-36.		H0658: 2		
HPDQO05	929274	640	588 - 875	3327	Ala-13 to His-22, Leu-80 to Arg-86.		L0520: 2, L0770: 2, H0658: 2, L0659: 1 and L0759: 1.		
HPDRB01	914437	641	306 - 449	3328			L0749: 3, H0658: 2 and H0660: 1.		
HPDRD28	957791	642	308 - 511	3329			H0658: 2, L0745: 2, H0644: 1 and L0529: 1.		
HPDRG92	967704	643	1 - 291	3330	Pro-51 to Phe-57, Ser-87 to Thr-94.		H0658: 2		
HPDRO20	957678	644	2 - 163	3331			L0021: 1, H0658: 1 and H0672: 1.		
HPDVB07	951634	645	342 - 554	3332	Arg-5 to Cys-10, Ser-22 to Ile-28.		H0644: 2 and H0658: 1.		
HPDVE05	928647	646	430 - 765	3333	Pro-22 to Asn-33, Arg-103 to Val-108.		L0512: 5, L0513: 4, H0686: 3, L0509: 3, L0789: 3, L0761: 2, L0772: 2, L0764: 2, L0717: 1, L0800: 1, L0378: 1, L0776: 1, L0659: 1, H0658: 1 and L0747: 1.		
HPDVF03	922193	647	524 - 847	3334			H0046: 2, L0794: 1, L0766: 1, H0658: 1, L0748: 1 and L0758: 1.		
HPDVK12	968977	648	97 - 243	3335			L0374: 1, L0804: 1, L0805: 1, H0658: 1, H0648: 1, L0750: 1 and		

HPDVM06	933443	649	439 - 591	3336	His-19 to Tyr-34, Glu-39 to Pro-47.	L0755: 1.		
HPDVY17	955902	650	226 - 444	3337	Gln-1 to Thr-6, Ser-22 to Leu-27, Ser-32 to Phe-37.	L0779: 2, H0032: 1 and H0658: 1. H0658: 2		
HPEAF19	867892	651	3 - 224	3338		H0165: 2		
HPEBA06	960802	652	253 - 2	3339	Trp-1 to Pro-11, Ala-27 to Phe-34, Ser-46 to Thr-60.	H0166: 1, H0059: 1 and L0768: 1.		
HPEBA51	723298	653	61 - 255	3340	Ile-18 to Asn-25.	H0166: 2 and L0598: 1.		
HPEBD31	655760	654	3 - 200	3341		H0166: 2 and L0604: 1.		
HPEBE44	716911	655	284 - 406	3342	Glu-31 to Cys-39.	H0166: 1, H0673: 1, L0763: 1 and L0581: 1.		
HPEKG18	914115	656	1 - 96	3343		H0673: 2		
HPEKJ42	922391	657	57 - 131	3344		H0673: 2		
HPEKU27	921663	658	220 - 408	3345		H0328: 1 and H0673: 1.		
HPEKX12	969251	659	2 - 217	3346	Gly-1 to Asn-8, Pro-22 to Ser-31, Thr-41 to Lys-48.	L0779: 2, H0428: 1, H0673: 1, L0766: 1 and L0658: 1.		
HPFAA06	960801	660	283 - 426	3347		H0168: 1 and H0169: 1.		
HPFCA36	524720	661	40 - 288	3348	Ser-12 to Ser-17, Lys-24 to Ser-34.	H0169: 2	6p21.1-p21.3	106300, 108800, 120290, 120290,

120810, 120820, 142857, 142858, 150270, 167250, 170261, 177900, 179450, 179605, 179605, 179605, 179605, 179605, 180297, 201910, 217000, 222100, 233100, 235200, 248611, 256550, 256550, 263200, 600202, 600261, 600364, 601498, 601690, 601868,								
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[illegible]

HPFCT09	655563	677	13 - 120	3364	Glu-21 to Pro-26.				
HPFCT53	974257	678	271 - 522	3365	Met-1 to Cys-9.	H0169: 2			
					Ile-3 to Ala-14,	H0169: 3			
HPFCT62	655432	679	82 - 198	3366	Arg-63 to Pro-68.				
					Glu-9 to Arg-15,	H0169: 2			
HPFCV19	655706	680	79 - 195	3367	Pro-24 to Tyr-39.				
					Leu-5 to Ser-11,	H0169: 2 and L0776:			
HPFCV71	525554	681	1 - 240	3368	Pro-13 to His-19,	1.			
					Lys-34 to Tyr-39.				
					Gly-22 to Cys-32.	H0328: 1, H0615: 1,			
HPFCX18	655588	682	153 - 263	3369		H0169: 1, L0807: 1 and			
HPFDD06	960700	683	2 - 163	3370	Ser-16 to Asp-26.	L0754: 1.			
HPFDE38	655704	684	67 - 330	3371	Lys-23 to Val-34.	H0169: 2			
					Leu-4 to Lys-18,	H0169: 2 and L0809:			
HPFDE61	974249	685	392 - 538	3372	Gly-36 to Glu-45,	1.			
					Lys-60 to Cys-65.				
					Asp-1 to Arg-7,	H0169: 4			
					Thr-17 to Asn-22,				
					Leu-25 to Pro-30.				
HPFDF79	973732	686	156 - 320	3373	Ser-3 to Tyr-9.	H0169: 3			
HPFDG58	655610	687	121 - 318	3374	Cys-32 to Pro-38.	H0169: 2			
HPFDI23	655549	688	197 - 367	3375	Leu-5 to Gly-10.	H0169: 2			
HPFDL90	954333	689	2 - 202	3376		H0169: 2			
HPFDS59	655543	690	8 - 160	3377		H0169: 2			
HPFDT17	581133	691	166 - 342	3378	Pro-18 to Asn-25.	H0169: 2			
HPFDT54	655530	692	36 - 212	3379		H0169: 2 and L0763:			
						1.			
HPFDT61	974569	693	63 - 173	3380		H0169: 3			

HPFDU30	522113	694	2 - 232	3381	His-46 to Pro-51.	H0169: 2		
HPFDU38	867879	695	36 - 167	3382		H0169: 2		
HPFDU59	739617	696	214 - 369	3383		H0169: 2		
HPFDV71	867870	697	124 - 354	3384	Pro-14 to Gly-25.	AR050: 117, AR054: 88, AR051: 81 H0169: 2		
HPFDX13	655571	698	1 - 294	3385	Val-1 to Lys-11, Pro-24 to Asp-33, Lys-44 to Glu-58.	H0169: 2, L0747: 2, H0688: 1, L0770: 1, L0803: 1, L0748: 1 and L0756: 1.		
HPFDZ20	655764	699	25 - 213	3386		H0169: 2		
HPFEA08	960372	700	2 - 187	3387	Ile-1 to Gly-44.	H0169: 3		
HPFEA32	925499	701	142 - 309	3388		H0169: 2		
HPFMA06	953536	702	63 - 212	3389	Ala-7 to Arg-12.	H0674: 2		
HPFML02	917775	703	39 - 113	3390	Lys-9 to Leu-15.	H0674: 2		
HPIAE79	655748	704	17 - 394	3391	Asn-1 to Lys-7, Pro-14 to Cys-23.	S0150: 2		
HPIAO83	655595	705	2 - 334	3392	Ser-1 to Arg-7, Pro-57 to Trp-67, Pro-70 to Ala-75, Ser-87 to Gly-95.	S0150: 2		
HPIAQ49	919469	706	106 - 243	3393	Pro-39 to Glu-46.	S0150: 2		
HPIAQ76	655573	707	61 - 2	3394	Lys-1 to Lys-17.	S0150: 2		
HPIAS40	928614	708	2 - 463	3395	Gly-1 to Val-6, Asp-25 to Gln-42.	H0484: 1 and S0150: 1.		
HPIAV80	615007	709	64 - 174	3396	Ser-8 to His-16.	S0150: 2		
HPIAX11	925424	710	282 - 608	3397		AR061: 9, AR089: 7 H0616: 1, S0150: 1 and L0581: 1.		



HPJAZ37	655753	711	2 - 289	3398		S0150: 2		
HPJBQ37	884289	712	2 - 424	3399	Ile-47 to Val-53, Phe-71 to Thr-76, Ser-105 to Thr-113, Glu-121 to Ser-129.	AR089: 4, AR061: 2 S0150: 2		
HPIBR51	725539	713	1 - 468	3400	Ala-15 to Ser-21, Gln-30 to Asp-36.	H0546: 1 and S0150: 1.		
HPIBT49	655719	714	176 - 283	3401	Tyr-30 to Cys-36.	S0150: 2		
HPIBY65	655757	715	133 - 294	3402		S0150: 2		
HPICC89	786117	716	211 - 414	3403		L0439: 2, H0616: 1 and S0150: 1.		
HPJAB19	655540	717	1 - 153	3404		S0152: 2		
HPJAB84	655531	718	3 - 269	3405	His-1 to Asp-6, Ala-16 to Ala-25.	S0152: 2		
HPJAC36	655601	719	154 - 330	3406	Cys-5 to Gly-12, Ser-47 to Arg-52.	S0152: 2 and L0780: 1.		
HPJAC92	867831	720	3 - 251	3407	His-1 to Leu-19.	S0152: 2		
HPJAD09	655712	721	180 - 332	3408		S0152: 2		
HPJAD66	655694	722	141 - 290	3409	Val-2 to Ser-14, Gly-27 to Ala-37.	S0152: 2		
HPJAD82	655765	723	53 - 187	3410	Arg-5 to Lys-13, Ser-20 to Thr-25.	S0152: 2		
HPJAV07	952852	724	180 - 335	3411	Leu-43 to Cys-51.	S0152: 2		
HPJAW56	823393	725	346 - 594	3412		L0748: 3, S0152: 2, H0615: 1, H0617: 1 and L0758: 1.		
HPJBI17	655761	726	162 - 326	3413	Ser-29 to Arg-35.	S0152: 2		
HPJBI89	655708	727	1 - 81	3414	Ser-19 to Gln-25.	S0152: 2		
HPJBK52	655751	728	99 - 263	3415		S0152: 2		

HPJBU08	958979	729	29 - 193	3416	Gln-13 to Thr-18, His-40 to Met-45.	S0152: 2		
HPJBV17	655729	730	10 - 123	3417		S0152: 2		
HPJCC04	926787	731	32 - 370	3418	Asn-42 to Gly-51.	S0152: 2		
HPJCP10	964259	732	113 - 244	3419		S0152: 2		
HPJCP11	966676	733	95 - 337	3420	Pro-36 to Gly-62.	H0056: 1 and S0152: 1.		
HPJCS84	590404	734	2 - 286	3421		S0152: 2		
HPJCV50	968095	735	260 - 460	3422	Ala-14 to Lys-21, Asp-37 to Gly-48, Gly-60 to Leu-65.	H0253: 1 and S0152: 1.		
HPJCX15	655730	736	245 - 334	3423		S0152: 2		
HPJCX26	655600	737	239 - 349	3424		S0152: 2		
HPJCY70	655569	738	111 - 203	3425	Pro-3 to Cys-11.	S0152: 2		
HPJCZ03	922850	739	79 - 183	3426	Val-2 to Thr-8.	S0152: 2		
HPJCZ06	934170	740	102 - 242	3427	Ser-1 to Gly-16.	S0152: 2		
HPJDA08	958182	741	438 - 1031	3428	Leu-8 to Lys-19, Asp-25 to Arg-33, Ser-40 to Ser-63, Ala-70 to Val-77, Glu-91 to Asp-97, His-108 to Asn-116, Lys-130 to Glu-136, Asp-139 to Val-144.	S0152: 2 and L0070: 1.		
HPJDJ58	906904	742	386 - 556	3429		S0152: 2		
HPJDP05	931027	743	299 - 454	3430		H0615: 2 and S0152: 1.		
HPJDY94	838748	744	79 - 183	3431		S0152: 2		
HPJEE38	954970	745	292 - 483	3432	Ser-23 to Arg-28.	L0770: 2, L0779: 2, H0553: 1, L0766: 1, L0666: 1, S0152: 1 and		

HPJEI55	926815	746	14 - 130	3433	Gly-1 to Pro-7.	L0777: 1.	
HPJEJ39	930988	747	284 - 538	3434	Gly-1 to Ala-11.	S0152: 2	
HPJEQ04	927618	748	149 - 328	3435		S0152: 2	
HPJEQ22	867725	749	239 - 448	3436	Thr-29 to Gly-38.	H0435: 1 and S0152: 1,11	
HPJET90	836503	750	39 - 377	3437	His-8 to Gly-18, Leu-40 to Ile-45, Asn-100 to Asp-105.	S0152: 2	
HPJEV06	934096	751	70 - 213	3438	Leu-17 to Glu-23, Arg-27 to Glu-35.	AR061: 0, AR089: 0 S0152: 2	
HPLAN47	717680	752	49 - 189	3439	Gly-1 to Arg-9.	S0152: 2	
HPLAR41	557554	753	236 - 3	3440		L0754: 39, L0748: 7, H0553: 4, H0030: 1, L0142: 1 and S0454: 1.	
HPLBB50	503751	754	287 - 72	3441		H0030: 2	
HPLBL31	503732	755	16 - 183	3442	Gly-1 to Ala-7, Pro-42 to Asn-47.	H0030: 2	
HPLBL57	503730	756	57 - 245	3443	Phe-29 to Lys-35.	H0030: 2	
HPLBO61	558187	757	2 - 241	3444	Glu-1 to Thr-9.	H0030: 1, H0038: 1 and L0758: 1.	
HPMAG19	705471	758	40 - 153	3445		H0031: 2	
HPMAH75	766443	759	2 - 214	3446		H0031: 2	
HPMBK34	954057	760	1 - 147	3447		H0031: 2	
HPMBK49	577661	761	125 - 301	3448	Gln-20 to Ser-31, Phe-41 to Gly-47.	H0031: 2 and L0777: 2.	
HPMBM48	575626	762	3 - 503	3449	Tyr-19 to Gly-46, Ser-48 to His-59, Gly-65 to Gly-77, Thr-91 to Tyr-96.	H0031: 3	

HPMBN02	920865	763	1 - 120	3450			H0031: 2		
HPMBO10	968365	764	39 - 278	3451			H0031: 4		
HPMBO61	867677	765	1 - 249	3452		Gly-1 to Gly-8.	H0031: 3		
HPMBR17	785732	766	192 - 404	3453		Thr-1 to Gln-7, Pro-24 to Gly-32.	H0031: 2		
HPMBU81	557870	767	28 - 165	3454		Ser-32 to Thr-41.	H0031: 2		
HPMBX35	531058	768	3 - 125	3455			H0031: 2		
HPMBX79	577637	769	118 - 276	3456			H0031: 2		
HPMBY76	531338	770	2 - 163	3457		Tyr-25 to Gly-32.	H0031: 2		
HPMBY83	527006	771	90 - 341	3458		Ser-50 to Gly-55.	H0031: 4 and L0803: 12		
HPMBZ05	932527	772	62 - 196	3459			H0031: 2		
HPMCB65	531289	773	111 - 302	3460		Gly-12 to Ile-18.	H0031: 2 and L0605: 1.		
HPMCC73	531066	774	171 - 314	3461		Pro-28 to Pro-42.	H0031: 2		
HPMCD77	529960	775	3 - 278	3462		Asp-1 to Cys-6.	H0253: 1 and H0031: 1.		
HPMCI02	381961	776	326 - 66	3463		Leu-19 to Thr-25, Arg-66 to Phe-87.	H0031: 2, L0809: 1, L0438: 1 and L0439: 1.		
	881473	2656	3 - 341	5343					
HPMCI65	577598	777	27 - 161	3464			H0031: 2		
HPMCJ14	524768	778	93 - 317	3465		Glu-30 to Asp-40.	H0031: 3		
HPMCJ19	531279	779	1 - 243	3466			H0031: 2		
HPMCJ48	577601	780	44 - 304	3467			H0031: 2		
HPMCK65	742095	781	54 - 314	3468		Leu-6 to Leu-16, Thr-24 to Trp-29.	H0031: 2 and L0600: 1.		
HPMCS19	954056	782	3 - 182	3469		Gln-1 to Gln-9, Arg-15 to Gly-22.	H0031: 3		
HPMCS65	961250	783	16 - 108	3470		Tyr-1 to Arg-8.	H0031: 10		

HPMCV93	657532	784	31 - 186	3471	Arg-5 to Trp-15.	H0031: 3 and L0594: 1.		
HPMCW25	867673	785	1 - 285	3472	Gly-1 to Ser-8, Leu-36 to Gly-42, Leu-48 to Asn-55, Lys-83 to Met-91.	H0031: 2 and L0758: 1.		
HPMCW53	727392	786	2 - 202	3473	Pro-19 to Lys-26, Pro-36 to Gly-55.	H0031: 2		
HPMCX11	967655	787	115 - 312	3474	Gln-6 to Thr-19.	H0031: 2 and L0662: 1.		
HPMCY30	867687	788	119 - 271	3475	Asp-7 to Leu-12, Ala-16 to His-21.	H0031: 2		
HPMCY31	725180	789	189 - 338	3476		H0031: 2		
HPMCY35	571411	790	272 - 397	3477		H0031: 3, L0667: 1 and L0748: 1.		
HPMDJ09	582594	791	108 - 215	3478		H0031: 4		
HPMDL78	577590	792	49 - 330	3479	Glu-1 to Pro-6, Thr-45 to Val-50.	H0031: 2		
HPMDO39	531275	793	55 - 204	3480		H0031: 2		
HPMDR07	867682	794	33 - 227	3481		H0031: 2		
HPMDT91	745346	795	3 - 299	3482	Gly-38 to Ser-45, Gly-72 to Gly-78.	H0031: 2		
HPMDU19	577626	796	163 - 276	3483		L0748: 14, H0553: 4, L0754: 4, H0644: 3, H0031: 2, L0005: 1, L0774: 1, S0454: 1, L0749: 1 and L0780: 1.		
HPMDY82	531274	797	7 - 51	3484	Lys-8 to Lys-15.	H0031: 2		
HPMDZ62	531276	798	116 - 286	3485	Phe-5 to Gly-10.	H0031: 2 and H0644:		

HPMEB66	531349	799	3 - 149	3486	Lys-20 to Thr-31.	1.			
HPMEC16	867658	800	136 - 249	3487		H0031: 2			
HPMEC36	668897	801	92 - 214	3488		H0031: 2			
HPMEC69	702501	802	1 - 114	3489	Ile-29 to Ile-36.	H0031: 2 and L0740: 1.			
HPMED52	531347	803	2 - 451	3490	Lys-23 to Ser-33.	AR061: 6, AR089: 3 H0031: 3			
HPMEE48	531321	804	240 - 437	3491		H0031: 4			
HPMEE66	577619	805	182 - 319	3492		H0031: 2			
HPMEG50	925080	806	3 - 122	3493	Pro-20 to Pro-26.	H0031: 2			
HPMEI39	784781	807	117 - 443	3494	Arg-1 to Ser-8, Pro-23 to Gly-30, Glu-62 to Arg-68.	H0031: 3, L0731: 3, H0046: 2, L0617: 1, L0747: 1 and L0779: 1.	22q12-q13	102480, 123620, 133450, 133450, 138981, 188826, 190040, 190040, 190040, 600850, 601669, 602229	
HPMFB02	920308	808	3 - 404	3495	Pro-15 to Leu-27, Phe-44 to Asp-49, Ala-83 to Lys-99.	H0031: 2	4q31.1-q31.2	189800, 600983	
HPMFB28	575934	809	3 - 281	3496	Asp-37 to Thr-43, Ala-46 to Ala-53, His-64 to Trp-76.	H0031: 3			

HPMFB37	575620	810	277 - 465	3497		H0031: 8 and L0581: 2.		
HPMFB75	526594	811	46 - 234	3498		H0031: 2		
HPMFB84	577593	812	148 - 291	3499	Leu-2 to Glu-8, Pro-39 to Ser-44.	H0031: 2		
HPMFE35	577633	813	3 - 158	3500	Gln-14 to Thr-22.	H0031: 2		
HPMFE60	577636	814	2 - 214	3501	Ser-8 to Ser-14, Ser-27 to Pro-48.	H0031: 2		
HPMFE73	575941	815	1 - 183	3502	Pro-38 to Gly-45.	H0031: 2		
HPMFH21	575943	816	248 - 460	3503		H0031: 2		
HPMFJ50	575932	817	170 - 487	3504	Gln-7 to Ser-12.	H0031: 2, L0438: 2 and L0439: 2.		
HPMFJ55	577588	818	53 - 259	3505		H0031: 5		
HPMFL08	959569	819	191 - 346	3506	Met-43 to Trp-52.	AR089: 1, AR061: 1 H0031: 2		
HPMFL80	874359	820	2 - 205	3507	Ala-1 to Lys-6, Pro-12 to Trp-19, Met-63 to Lys-68.	H0031: 2, H0644: 1 and L0527: 1.		
HPMFM29	582595	821	482 - 631	3508		H0428: 1, H0031: 1, L0766: 1, L0659: 1, H0690: 1, L0439: 1, L0754: 1 and L0756: 1.		
HPMFN12	968821	822	262 - 444	3509	Arg-15 to Val-21.	H0031: 3		
HPMFP05	867662	823	107 - 427	3510	Leu-9 to Ile-17.	H0031: 2		
HPMFP30	577629	824	121 - 348	3511		H0031: 3		
HPMFP38	575914	825	118 - 261	3512		H0031: 3		
HPMFQ84	867651	826	483 - 692	3513		H0031: 4 and L0754: 1.		
HPMFS41	711640	827	64 - 342	3514	Ala-1 to Asn-9,	H0031: 3		

HPMFT04	916662	828	28 - 180	3515	Glu-17 to Glu-22, Trp-36 to Gln-44.	H0031: 4	
HPMFU89	575894	829	169 - 300	3516	Tyr-24 to His-32.	H0031: 2	
HPMFV28	652097	830	172 - 312	3517	Lys-1 to Gly-7.	H0031: 2	
HPMFV82	575911	831	57 - 167	3518	Phe-15 to Asn-20.	H0031: 2	
HPMFV88	956263	832	204 - 365	3519	Gln-10 to Gln-20.	H0031: 2	
HPMFW25	960065	833	16 - 246	3520	Arg-18 to Val-24, Glu-43 to Gly-54.	H0031: 2	
HPMFW78	932529	834	3 - 152	3521	Asp-19 to Ser-30.	H0031: 5 and L0142: 1.	
HPMFX13	575908	835	284 - 412	3522	Leu-34 to Cys-41.	L0774: 4, H0031: 2, L0439: 2, L0435: 1, L0803: 1 and H0670: 1.	
HPMFX65	867657	836	158 - 355	3523		H0031: 2	
HPMFX70	577642	837	3 - 218	3524	His-1 to His-7, Ser-16 to Glu-22, Phe-65 to Ser-71.	H0031: 2	
HPMFX92	577603	838	3 - 206	3525	Arg-28 to Leu-37.	H0031: 2	
HPMGA83	968359	839	88 - 243	3526	His-39 to Thr-44.	H0031: 4	
HPMGB22	506379	840	180 - 320	3527		H0031: 2	
HPMGC07	920313	841	55 - 381	3528	Gln-6 to Trp-17.	H0031: 9 and L0758: 1.	
HPMGC23	703835	842	1 - 306	3529	Arg-18 to Ser-29, Gly-62 to Tyr-78.	H0031: 2	
HPMGE31	867648	843	30 - 353	3530		H0031: 2	
HPMGE95	873392	844	176 - 340	3531		H0031: 3	
HPMGF06	954823	845	1 - 564	3532	Gly-1 to Ser-16, Ser-37 to Lys-42,	H0031: 3, H0651: 1, L0731: 1 and L0758: 1.	



HPMGF32	577615	846	226 - 92	3533	Arg-44 to Val-50. Tyr-1 to Ile-7, Cys-20 to Asp-33, Leu-40 to Ser-45.	H0031: 2			
HPMGH16	577641	847	267 - 398	3534		H0031: 2			
HPMGI03	924521	848	62 - 283	3535		H0031: 2	20		
HPMGI84	920326	849	79 - 219	3536		H0031: 3			
HPMGJ93	864040	850	147 - 359	3537	Trp-40 to His-45.	H0031: 2			
HPMGK37	575924	851	223 - 369	3538		H0031: 2			
HPMGK59	671936	852	159 - 488	3539	His-18 to Cys-23, Glu-33 to Phe-40, Thr-42 to Trp-47, Cys-53 to Glu-63.	H0031: 3, L0757: 3, L0803: 2 and L0766: 1.			
HPMGK62	730751	853	347 - 529	3540		H0031: 3 and L0754: 1.			
HPMGM33	854081	854	2 - 223	3541	Ala-1 to Asn-16, Lys-45 to Thr-54.	L0805: 5, H0031: 2, L0749: 2, L0766: 1, L0776: 1 and L0779: 1.			
HPMGM54	577599	855	189 - 356	3542		H0031: 2			
HPMGR80	506235	856	24 - 224	3543		H0031: 2	7p15-p12	138079, 138079, 139191, 142959, 153880, 180104, 600994, 601649	
HPMGGS09	575951	857	46 - 111	3544		H0031: 2			
HPMGGS24	796440	858	230 - 367	3545		H0031: 2			

HPMGT67	970815	859	1 - 123	3546	Ser-26 to Trp-32.	H0031: 2	
HPMGV12	968364	860	35 - 301	3547	His-1 to Glu-6.	H0031: 2	
HPMGV15	582596	861	88 - 210	3548		H0031: 4	
HPMGV59	577635	862	38 - 277	3549	Asp-23 to Pro-34.	H0031: 2	
HPMGW48	920309	863	3 - 257	3550	His-1 to Gln-15, Arg-37 to Asp-48, Ser-63 to Pro-77, Gly-79 to Lys-85.	H0031: 2	
HPMGX23	575903	864	3 - 314	3551	Ser-2 to Pro-27, Leu-38 to Asn-52.	H0031: 2	19q12
HPMHA80	970813	865	142 - 294	3552		H0031: 2	
HPMHB74	577595	866	289 - 552	3553	Lys-31 to Thr-37.	H0031: 2, L0769: 1 and L0439: 1.	
HPMHB83	531382	867	1 - 147	3554	Gly-1 to Ser-8, Ile-41 to Ile-49.	H0031: 3	
HPMHC74	577631	868	46 - 198	3555		H0031: 2	
HPMHD66	928433	869	1 - 441	3556	Arg-13 to Ala-23, Met-27 to Gly-36, Ser-109 to Leu-116.	H0031: 2	
HPMHD71	760426	870	159 - 1	3557	Arg-1 to Thr-20.	H0031: 3	
HPMJC01	914759	871	1 - 267	3558		H0031: 1 and H0644: 1.	
HPMJC05	930844	872	2 - 370	3559	Leu-39 to Ser-46, Gly-87 to Pro-94.	H0644: 2	
HPMJD88	930806	873	136 - 330	3560	Gln-42 to Asp-50.	H0644: 3	
HPMJB84	867587	874	207 - 425	3561	Ile-1 to Gln-10, Ser-20 to Gln-27.	H0644: 2	
HPMJF76	965642	875	1 - 171	3562		H0644: 2	
HPMJJ81	930873	876	166 - 276	3563	Glu-15 to Arg-20.	H0644: 2 and H0615:	

HPMJN59	946876	877	84 - 470	3564		1.	AR089: 21, AR061: 15 H0644: 2			
HPMJO46	922649	878	1 - 222	3565	Ala-1 to Phe-6, Thr-32 to Gly-38, Pro-54 to Gln-73.	H0644: 2				
HPMJR02	917419	879	160 - 429	3566	Arg-37 to Asn-50, His-81 to Gln-89.	H0644: 2				
HPMJV08	958001	880	204 - 353	3567	Tyr-15 to Tyr-21.	H0644: 3				
HPMJY55	922657	881	3 - 203	3568		H0644: 3				
HPMKB19	969478	882	287 - 454	3569	Ser-8 to Phe-26.	H0644: 2, L0794: 1 and L0748: 1.				
HPMKI53	957997	883	3 - 125	3570		H0644: 2				
HPMKM81	894416	884	64 - 567	3571	Arg-15 to Gln-21, Gln-47 to Ile-53, Lys-58 to Asp-72.	AR061: 2, AR089: 1 L0666: 3, L0777: 2, L0608: 2, H0046: 1, H0031: 1, H0644: 1, L0803: 1, L0783: 1, H0672: 1, L0740: 1, L0750: 1 and L0755: 1.	7q22	126650, 126650, 154276, 173360, 173360, 602136, 602136, 602136, 602447		
HPMKN43	867573	885	222 - 545	3572	Arg-2 to Tyr-7.	H0644: 2 and L0589: 1.				
HPMLE04	867533	886	343 - 543	3573		H0644: 3 and L0471: 1.				
HPMLK02	918123	887	173 - 421	3574	Leu-36 to Gln-52.	H0644: 2 and L0527: 1.				
HPMLK76	922621	888	155 - 370	3575	Arg-43 to Ser-48.	H0644: 2				

HPMLL74	953069	889	1 - 285	3576	Gly-4 to Ser-11.	H0544: 1, H0644: 1 and L0754: 1.		
HPMLW10	963037	890	53 - 211	3577		H0644: 2		
HPMSF86	509490	891	44 - 226	3578	Ser-8 to His-17.	H0111: 2		
HPRAE13	971652	892	3 - 329	3579	Gly-8 to Glu-21, Val-23 to Ser-37.	H0032: 2 and L0759: 1.		
HPRAN84	585489	893	87 - 299	3580	Cys-19 to Ser-29, Ser-31 to Gly-37, His-48 to Gln-53.	H0032: 2		
HPRAU45	536630	894	191 - 27	3581	Ser-12 to Gln-18, Arg-23 to Gly-30.	H0032: 2		
HPRAZ10	968692	895	1 - 183	3582	Gln-13 to Ile-22, Val-34 to Ser-39.	L0758: 2, H0688: 1 and H0032: 1.		
HPRBA65	655537	896	98 - 241	3583	Arg-23 to Glu-35.	H0032: 2		
HPRBE36	655587	897	91 - 330	3584	Ile-6 to His-11, Gly-24 to Val-29.	H0032: 2		
HPRBL91	655693	898	192 - 299	3585		H0032: 2		
HPRCB11	960316	899	178 - 336	3586	Ser-13 to Asn-20.	H0032: 2		
HPRCB21	655725	900	2 - 121	3587	Ser-19 to Ser-25.	H0032: 2		
HPRCC08	939490	901	3 - 296	3588	Leu-39 to Ile-47.	H0032: 2		
HPRCC61	964909	902	3 - 176	3589		H0032: 2		
HPRCN41	655554	903	23 - 169	3590		H0032: 2		
HPRCU13	968521	904	156 - 269	3591		H0032: 2		
HPRSB16	666295	905	3 - 188	3592		H0211: 2		
HPRTL26	849081	906	258 - 419	3593	Gln-1 to Gly-7, Thr-22 to Gly-31.	H0212: 2 and H0032: 1.		
HPRTP73	708761	907	127 - 273	3594		H0032: 1 and H0212: 1.		
HPVAB11	967944	908	295 - 495	3595	Arg-8 to Phe-20,	L0777: 3, L0662: 1, 20		

HPVAF49	655578	909	108 - 287	3596	Gly-36 to Lys-42.	L0803: 1, L0787: 1, H0672: 1, S0013: 1 and L0747: 1.
HPVAF69	753744	910	2 - 145	3597	Arg-4 to Ser-20, Lys-50 to Glu-60. Ile-22 to Asn-28.	S0013: 2
HPVAH36	525537	911	204 - 362	3598	Ser-3 to Gly-11, Thr-42 to Gly-52.	L0662: 1, L0774: 1, L0659: 1, H0672: 1, S0013: 1 and L0754: 1.
HPWAF85	655691	912	116 - 550	3599	Arg-39 to Asp-55, Ala-93 to Ser-99, Pro-102 to Ser-111.	T0069: 1 and S0013: 1.
HPWAH48	655527	913	19 - 156	3600	Asn-6 to Trp-17.	S0044: 2 and H0618: 1.19q
HPWAS77	908450	914	655 - 266	3601	His-18 to Pro-24.	S0044: 2
HPWBA33	655733	915	66 - 227	3602	Ala-7 to Thr-13, Arg-43 to Arg-49.	AR061: 7, AR089: 3 S0044: 2, L0747: 2, L0777: 2 and L0480: 1.
HPWBO84	867289	916	14 - 289	3603	Arg-44 to His-50, Gln-62 to Arg-69, Gln-80 to Trp-87.	S0044: 2
HPWCA53	657484	917	197 - 367	3604	Phe-24 to Thr-29.	S0044: 2
HPWCJ27	655614	918	2 - 157	3605	Glu-10 to Gln-19, Gln-22 to Lys-27, Pro-37 to Val-44.	S0044: 2
HPWCJ67	655560	919	236 - 373	3606	Leu-4 to Lys-9.	S0044: 2
HPWCJ82	655577	920	215 - 415	3607	Ser-15 to Ser-22.	S0044: 2
HPWDA73	514113	921	513 - 656	3608	Leu-43 to Leu-48.	S0044: 1 and S0396: 1.

	716228	2657	53 - 373	5344					
HPWDA86	961529	922	15 - 164	3609	Gln-1 to Gly-8, Lys-15 to Ser-23.			H0648: 1 and S0044: 1.	
HPWDD72	537333	923	193 - 342	3610				S0044: 2 and L0748: 1.	
HPWSB35	655713	924	74 - 268	3611				S0174: 2	
HPZAB38	655591	925	138 - 254	3612				S0168: 2	
HSWAC73	710354	926	2 - 409	3613				H0618: 1, H0546: 1 and H0040: 1.	
HSWAD39	705322	927	638 - 489	3614				L0777: 3, H0546: 2, L0803: 2, L0755: 2, L0637: 1, L0662: 1, L0794: 1, H0659: 1 and L0758: 1.	
HSWBD86	785439	928	1 - 150	3615	Ser-13 to Ser-19, Arg-37 to Gly-48.			L0800: 2, L0764: 2, L0779: 2, H0546: 1, L0351: 1, L0769: 1, L0771: 1, L0438: 1, H0660: 1, L0439: 1 and L0592: 1.	
HSWBJ40	711066	929	2 - 307	3616				L0731: 3, H0545: 2, L0744: 2, L0021: 1, H0546: 1, L0769: 1, L0666: 1 and L0665: 1.	
HSWBO34	868007	930	611 - 826	3617	Gln-1 to Phe-10.			L0777: 2, L0005: 1, H0546: 1, H0328: 1, L0761: 1, L0373: 1, L0527: 1, L0526: 1, L0754: 1, L0752: 1, L0755: 1, L0731: 1 and L0608: 1.	

HTEAA54	923070	931	34 - 513	3618	Gln-1 to Met-10, Met-16 to Lys-21, Thr-26 to Met-32.	H0618: 2, H0038: 1 and H0616: 1.		
HTEAB52	537136	932	1 - 315	3619	Pro-53 to Asn-59.	H0038: 3		
HTEAD32	504353	933	50 - 187	3620	Arg-16 to Thr-28.	H0038: 2		
HTEAD95	961232	934	1 - 246	3621	Cys-5 to Ser-11, Pro-13 to Thr-18, His-28 to Arg-33, Arg-40 to Arg-45, Pro-52 to Arg-57, His-66 to Gln-71.	H0038: 3, L0747: 2, H0618: 1, L0665: 1, L0779: 1 and L0758: 1.		
HTEAF07	835805	935	87 - 326	3622		L0758: 6, H0038: 3, H0616: 1, L0659: 1 and L0779: 1.		
	954433	2658	330 - 91	5345	Arg-1 to Pro-9.			
HTEAF26	537271	936	238 - 116	3623	Thr-5 to Glu-11.	H0038: 11, L0758: 7, L0753: 2 and H0616: 1.		
HTEAG50	787500	937	199 - 104	3624	Val-6 to Lys-13.	H0038: 1 and H0616: 1.		
HTEAK57	536769	938	423 - 202	3625		H0038: 12, H0616: 6, H0593: 1, L0439: 1 and L0756: 1.	10p12-p11.2 600964, 602026	
HTEAL28	963538	939	3 - 626	3626	Gln-11 to Lys-24, His-60 to Leu-67, Arg-85 to Ser-92.	H0038: 11, L0758: 7, L0753: 2 and H0616: 1.		
HTEAP91	966113	940	10 - 324	3627	Glu-13 to Trp-29, Thr-31 to Thr-44, Arg-54 to Ser-71.	H0616: 4, L0758: 2 and H0038: 1.		
HTEAR84	783328	941	2 - 130	3628		H0038: 1 and H0616: 1.		

HTEAV43	927010	942	368 - 520	3629	Lys-17 to Lys-26.	L0758: 3, H0616: 2 and H0038: 1.		
HTEAY67	679390	943	280 - 143	3630	Tyr-14 to Ser-19.	L0758: 3, H0038: 2, L0794: 2 and L0779: 1.		
HTEAZ54	793441	944	286 - 501	3631		H0038: 2 and H0616: 1.		
HTEBC74	887782	945	1 - 321	3632	Pro-32 to Asn-39.	AR054: 7, AR051: 2, AR089: 1, AR061: 0 L0663: 2, H0038: 1, H0672: 1 and L0779: 1.		
HTEBD35	967959	946	13 - 252	3633	Asn-28 to Cys-34.	H0038: 2		
HTEBD40	779134	947	3 - 152	3634	Pro-44 to Ser-50.	H0038: 2 and H0616: 1.		
HTEBJ78	779265	948	3 - 971	3635	Ser-86 to Thr-97, Gln-104 to Pro-116, Glu-168 to Ser-182, Thr-190 to Ser-198, Glu-208 to Tyr-213, Ser-230 to Val-237.	H0038: 7, H0253: 1, H0616: 1 and L0151: 1.		
HTEBP39	742218	949	373 - 540	3636	Glu-38 to Ala-46.	H0038: 2, H0328: 1 and H0616: 1.		
HTEBS30	693377	950	185 - 334	3637	Ser-39 to Val-49.	H0038: 2 and H0616: 2.		
HTEBS77	953904	951	106 - 552	3638	Lys-1 to Asn-14.	H0038: 1 and H0616: 1.		
HTEBS80	854052	952	201 - 359	3639	Lys-24 to Val-32.	H0038: 2, H0040: 2 and L0758: 1.		
HTEBX62	508150	953	250 - 417	3640		H0038: 2		
HTEBY08	960427	954	3 - 356	3641	Ile-11 to Trp-17,	AR061: 1, AR089: 0		



HTEBY15	526281	955	1 - 231	3642	Arg-52 to Glu-65.	H0038: 4		
HTEBY28	923026	956	1 - 546	3643	Lys-66 to Thr-72. Arg-1 to Phe-12, Met-34 to Lys-39, Lys-46 to Ser-56, Pro-72 to Lys-79, Lys-101 to Asp-107, Trp-139 to Lys-148.	H0038: 2 H0616: 3 and H0038: 2.		
HTEBY41	711523	957	106 - 243	3644		H0038: 2 and H0616: 1.		
HTEBY61	967340	958	1 - 435	3645	Glu-9 to Arg-24, Arg-32 to Thr-40.	H0253: 1, H0038: 1 and L0758: 1.		
HTEBZ21	958381	959	2 - 121	3646		H0038: 2 and H0616: 1.		
HTECA13	507053	960	1 - 204	3647	His-27 to Leu-39.	H0038: 4 and H0616: 1.		
HTECA16	764416	961	111 - 389	3648	Glu-8 to Lys-17.	H0038: 2 and L0779: 1.		
HTECA21	911369	962	1 - 387	3649	Asn-1 to His-6, Arg-117 to Cys-126.	AR061: 596, AR089: 427 H0038: 2, H0616: 1 and L0439: 1.		
HTECA32	947605	963	792 - 406	3650		AR061: 49, AR089: 45 H0038: 2		
HTECA51	708860	964	96 - 248	3651		H0038: 2, L0748: 2, L0749: 2, L0769: 1, L0776: 1, L0659: 1 and L0663: 1.		
HTECA83	870692	965	3 - 311	3652	Arg-22 to Tyr-28, Ser-78 to Arg-87.	H0038: 2		

HTECB21	921070	966	32 - 271	3653	Tyr-1 to Arg-6, Ile-49 to Val-55.	H0038: 3		
HTECC13	971673	967	61 - 270	3654		H0253: 1 and H0038: 1.		
HTECC20	963353	968	763 - 1005	3655	Arg-1 to Arg-11, Arg-55 to Ser-70, Ser-76 to Gly-81.	H0038: 2 and H0616: 2.		
HTECC37	508143	969	1 - 147	3656		H0038: 1 and H0616: 1.		
HTECC38	844558	970	203 - 463	3657	Arg-15 to Leu-21, Ala-29 to Glu-34.	H0038: 4, H0616: 3, L0758: 3 and L0779: 1.		
HTECC66	790937	971	84 - 287	3658	Asn-9 to Asn-16, Asp-60 to Lys-68.	H0038: 2 and H0616: 1.		
HTECC80	796820	972	37 - 459	3659	Gln-18 to Trp-29, Arg-46 to Val-52.	H0038: 2 and H0616: 1.		
HTECC85	508138	973	1 - 297	3660	Ala-10 to Thr-17, Glu-19 to Glu-28, Thr-36 to Trp-44, Ile-47 to Gly-54, Ala-61 to Pro-69.	H0038: 2		
HTECC96	959874	974	138 - 491	3661	Pro-6 to Cys-11, Pro-77 to His-92.	H0038: 2		
HTECD17	508108	975	154 - 411	3662		H0038: 2		
HTECD18	973163	976	2 - 508	3663	Arg-1 to Ala-35, Gly-41 to Lys-61.	H0616: 14, H0038: 12, H0618: 6, H0253: 5, L0758: 5, L0768: 4, H0411: 2, L0779: 2, L0151: 1, L0697: 1 and S0398: 1.		
HTECD36	518124	977	1 - 141	3664	Val-9 to His-36.	H0038: 2		

HTECD62	527207	978	3 - 161	3665	His-8 to Arg-15, Lys-19 to Lys-36.	H0038: 2, L0794: 2, L0779: 2, H0616: 1 and L0758: 1.		
HTECD75	727422	979	3 - 275	3666	Gly-2 to Ala-8, Pro-10 to Thr-18, Pro-23 to Ser-34, Pro-45 to Asp-55.	H0616: 4, H0038: 2 and L0758: 1.		
HTECE09	620494	980	2 - 286	3667	Ile-1 to Gly-9.	H0038: 2		
HTECE44	764830	981	2 - 286	3668	Ser-29 to Gly-35, Asp-85 to Val-92.	H0038: 8, L0758: 5, L0794: 4, H0616: 2, L0763: 1 and L0777: 1.		
HTECE45	790894	982	2 - 352	3669		L0766: 2, H0038: 1 and H0616: 1.		
HTECE69	522983	983	2 - 253	3670	Ile-1 to Arg-13, Glu-25 to Leu-31.	H0038: 2		
HTECE91	522984	984	3 - 296	3671		H0038: 2		
HTEDF13	522964	985	123 - 257	3672	Glu-1 to Thr-6, Glu-30 to Met-43.	H0038: 2		
HTEDF23	522966	986	3 - 164	3673	Gly-2 to Arg-19, Arg-24 to Gly-29, Lys-48 to Arg-54.	H0038: 2		
HTEDF57	964734	987	2 - 418	3674	Asn-37 to Val-42, Lys-82 to Glu-95, Glu-100 to Leu-105, Tyr-114 to Ser-120, Leu-129 to Lys-134.	H0616: 2 and H0038: 1.		
HTEDF76	522973	988	141 - 329	3675		H0038: 2		
HTEDG16	925527	989	1 - 423	3676	Gln-61 to Cys-76, Ile-95 to Asp-111.	H0038: 2		

HTEDG34	761752	990	169 - 324	3677			H0616: 2 and H0038: 1.		
HTEDH21	522764	991	3 - 170	3678	Arg-1 to Glu-9, Thr-42 to Arg-49.		H0038: 3		
HTEDH22	522765	992	33 - 206	3679			H0038: 2, H0616: 2, L0769: 1, L0794: 1, L0779: 1 and L0758: 1.		
HTEDH54	957762	993	1 - 411	3680	Asn-1 to Ser-14, Glu-103 to Gly-108.		H0038: 1 and H0616: 1.		
HTEDI02	921243	994	121 - 705	3681	Glu-7 to Lys-13, Asp-29 to Leu-34, His-83 to Pro-91, Ser-106 to Thr-111.		AR061: 14, AR089: 12 H0618: 2, H0634: 2, H0038: 1, H0616: 1 and L0758: 1.		
HTEDI16	932292	995	65 - 544	3682	Lys-18 to Arg-24, Pro-30 to Thr-35.		H0038: 2, H0616: 2, L0740: 1 and L0758: 1.		
HTEDI82	536477	996	274 - 549	3683	Pro-20 to Thr-29.		H0038: 3		
HTEDI04	519940	997	43 - 165	3684			H0038: 2		
HTEDI30	771404	998	3 - 305	3685			L0740: 2, H0615: 1, H0428: 1, H0038: 1, L0662: 1, L0805: 1, L0661: 1 and L0751: 1.		
HTEDM08	960303	999	3 - 257	3686	Pro-31 to Ala-40.		H0038: 2 and H0616: 1.	8p12-p11.2	136350, 152760, 173370, 180100, 182900, 185430, 270800, 277700, 600617

HTEDO31	870711	1000	101 - 271	3687	Pro-1 to Trp-9, Pro-25 to Lys-31.	H0038: 2	
HTEDO51	530592	1001	3 - 164	3688	Arg-8 to Ser-20.	H0038: 2	
HTEDO59	964379	1002	130 - 231	3689		H0553: 1 and H0038: 1.	
HTEDP15	870675	1003	1 - 321	3690		H0038: 4	
HTEDP31	870548	1004	68 - 337	3691		H0038: 1 and H0616: 1.	
HTEDP32	839532	1005	152 - 322	3692	Ser-9 to Ala-15.	H0038: 2	
HTEDP83	536821	1006	1 - 345	3693		H0038: 2	
HTEDQ30	530589	1007	3 - 206	3694		AR061: 7, AR089: 3 L0758: 4, H0038: 2 and H0616: 1.	
HTEDQ72	795332	1008	53 - 475	3695	Pro-11 to Cys-28, Ser-41 to Leu-55, Pro-58 to Asn-63, Phe-67 to Ser-77.	H0616: 2, H0038: 1 and L0758: 1.	
HTEDQ83	530586	1009	318 - 494	3696		H0038: 2	
HTEDR71	761585	1010	88 - 171	3697		L0070: 2, H0038: 1 and H0616: 1.	
HTEDR91	530451	1011	53 - 238	3698	Ala-25 to Thr-32, Lys-46 to Gly-52.	H0038: 2	
HTEDU45	870708	1012	137 - 706	3699	Ile-2 to Gly-8.	L0731: 6, L0758: 3, H0618: 1, H0038: 1 and L0794: 1.	
HTEDU48	932315	1013	2 - 730	3700	Lys-16 to Ser-22.	H0038: 2 and H0616: 2.	
HTEDV02	921114	1014	3 - 164	3701		H0038: 2	
HTEDX22	523959	1015	324 - 566	3702	Phe-37 to Ser-49.	H0038: 3, L0438: 2,	

HTEDX55	530452	1016	172 - 357	3703	Arg-1 to Asn-13, Met-37 to Pro-47.	H0616: 1 and L0439: 1. H0038: 2		
HTEDY38	771505	1017	3 - 140	3704	Lys-28 to Lys-41.	H0616: 2 and H0038: 1.		
HTEDY54	922964	1018	151 - 762	3705	Asp-67 to Asn-72, Pro-113 to Gly-121.	H0616: 3, L0759: 3, H0038: 1, L0774: 1 and L0777: 1.		
HTEDY57	530580	1019	189 - 326	3706	Glu-11 to Gln-18.	H0038: 2		
HTBEA03	925399	1020	86 - 199	3707	His-1 to His-10.	H0169: 2 and H0038: 1.		
HTEEB18	523962	1021	271 - 549	3708	Gln-9 to Asn-26.	H0038: 2 and L0779: 1.		
HTEEB33	924818	1022	100 - 615	3709	His-19 to Lys-55, Pro-72 to Ser-84, Ser-92 to Gly-104, Ser-111 to Asp-124, Thr-129 to His-141.	H0038: 5 and H0618: 1.		
HTEEC10	968517	1023	1 - 216	3710	Ser-1 to Gly-14, Lys-28 to Ser-37.	H0038: 2 and H0616: 1.		
HTEEE65	530157	1024	202 - 384	3711		H0038: 2, L0758: 2 and L0779: 1.		
HTEEF31	924840	1025	88 - 345	3712	Pro-5 to Gln-13, Thr-40 to Arg-45, Thr-52 to Gln-57, Phe-59 to Gly-64.	H0038: 2		
HTEEH31	507814	1026	72 - 215	3713	Glu-9 to Val-15, Glu-24 to Pro-30.	H0038: 3		
HTEEU23	524059	1027	2 - 328	3714	Pro-8 to Leu-13.	H0038: 2		

HTEEU52	530199	1028	128 - 343	3715	Pro-32 to Asp-39, Lys-57 to Gly-65.	H0038: 1 and H0616: 1.		
HTEEU88	698315	1029	106 - 240	3716	Ser-1 to Ser-8, Ser-11 to Trp-19.	H0038: 3		
HTEEU92	960127	1030	136 - 393	3717	Asn-2 to Lys-8, Lys-16 to Asp-23, Arg-28 to His-51.	H0038: 2 and L0779: 1.		
HTEEV53	523957	1031	48 - 311 -	3718	Pro-24 to Ala-38.	H0038: 2		
HTEEW73	917206	1032	55 - 507	3719		H0038: 4, L0779: 2, L0758: 2 and L0618: 1.		
HTEEZ95	530095	1033	1 - 147	3720		H0038: 2		
HTEFJ53	935982	1034	103 - 222	3721		H0038: 2		
HTEFM31	771355	1035	298 - 429	3722		H0616: 2 and H0038: 1.		
HTEFN15	959854	1036	266 - 493	3723		H0038: 2 and H0616: 1.		
HTEFO32	529272	1037	150 - 73	3724	Phe-3 to Val-24.	H0038: 2		
HTEFO76	770270	1038	240 - 416	3725		H0038: 1 and H0616: 1.		
HTEFP14	659369	1039	3 - 260	3726		H0038: 4 and H0616: 1.		
HTEFP50	507219	1040	124 - 321	3727	Met-41 to Ile-46.	L0776: 3 and H0038: 2.		
HTEFP61	711399	1041	119 - 352	3728	Arg-1 to Gln-22.	H0038: 3		
HTEFS60	836010	1042	1 - 168	3729		H0038: 1 and H0616: 1.		
HTEFU46	920604	1043	118 - 195	3730		H0038: 2		
HTEFW55	787550	1044	273 - 662	3731		H0616: 4 and H0038: 1.		

HTEFW56	528019	1045	35 - 358	3732	Arg-1 to Asp-7, Trp-24 to Cys-29, Ser-68 to Ile-73.	H0038: 2 and H0616: 1.		
HTEFW78	961061	1046	1 - 279	3733	Arg-3 to Leu-10, Gln-34 to Glu-41, Ile-48 to Ser-53.	H0038: 1 and H0616: 1.		
HTEFX53	842047	1047	268 - 35	3734	Lys-1 to Thr-6.	H0038: 3		
HTEGA13	656077	1048	2 - 139	3735		H0038: 3	2q37.3	
HTEGA17	964198	1049	2 - 1519	3736	Val-11 to Ser-19.	H0038: 15, L0758: 5, H0618: 1, H0253: 1, L0151: 1 and L0768: 1.		
HTEGA43	715583	1050	190 - 306	3737	Lys-7 to Tyr-19.	H0038: 2		
HTEGA47	503300	1051	2 - 298	3738	Lys-6 to Lys-16, Arg-44 to Gln-51, Asn-57 to Phe-63, Ser-84 to Trp-89.	H0038: 2, L0779: 2 and L0758: 2.		
HTEGD11	967698	1052	190 - 468	3739	Gln-6 to Ser-11, Ser-15 to Gly-31, Ser-69 to Lys-93.	H0038: 1 and H0616: 1.		
HTEGE44	528017	1053	2 - 334	3740	Asn-1 to Pro-9.	H0038: 2		
HTEGF78	614242	1054	210 - 407	3741	Thr-1 to Ala-7.	H0038: 2		
HTEGF95	796660	1055	76 - 267	3742	Glu-25 to Trp-31, Lys-49 to Ser-54.	H0038: 1 and H0616: 1.		
HTEGG07	954115	1056	144 - 335	3743		H0038: 2		
HTEGG61	528007	1057	2 - 217	3744		H0038: 2		
HTEGK51	520046	1058	3 - 143	3745	Pro-13 to Lys-25.	H0038: 2		
HTEGM38	675087	1059	84 - 263	3746	Ala-15 to Tyr-24, His-32 to Asp-39.	AR089: 1, AR061: 0 H0038: 2	11q25	602782
HTEGN63	520037	1060	1 - 183	3747	Asn-38 to Glu-47.	H0038: 2		



HTEGO05	932583	1061	3 - 884	3748	Pro-12 to Tyr-21.	AR089: 1, AR061: 0 H0038: 2, L0745: 2 and H0616: 1.		
HTEGQ21	923059	1062	134 - 433	3749	Lys-28 to Lys-34, Glu-42 to Ser-48, Ser-53 to Phe-63.	L0794: 15, H0616: 13, H0038: 7, H0253: 1 and L0758: 1.		
HTEGQ74	573865	1063	2 - 187	3750	Val-3 to Ser-8, Cys-35 to Lys-45.	H0038: 2		
HTEGR56	959871	1064	23 - 196	3751	Glu-8 to Ile-22.	H0038: 2		
HTEGR88	871611	1065	160 - 402	3752		H0038: 3		
HTEGS16	527914	1066	131 - 352	3753		H0038: 2		
HTEGS34	458520	1067	220 - 405	3754	Pro-35 to Glu-43, Gly-52 to His-57.	H0038: 2, L0758: 2, H0294: 1 and H0616: 1.		
HTEGS93	506653	1068	155 - 355	3755		H0038: 2		
HTEGT29	870638	1069	200 - 367	3756	Arg-1 to Thr-11.	H0038: 3 and L0758: 1.		
HTEGT33	716783	1070	170 - 463	3757		H0038: 2 and L0758: 2.		
HTEGU13	520041	1071	2 - 205	3758	Ala-1 to Tyr-14, Thr-28 to Ser-60.	H0038: 3 and H0616: 1.		
HTEGU32	524053	1072	39 - 506	3759	Asn-44 to Asp-49, Ala-91 to Thr-97.	H0253: 8, H0038: 2, H0179: 1, L0151: 1 and L0758: 1.		
HTEGU62	573885	1073	3 - 98	3760		H0038: 2 and H0616: 1.		
HTEGU93	764831	1074	194 - 595	3761		H0038: 8, L0758: 5, L0794: 4, H0616: 2, L0763: 1 and L0777: 1.		
HTEGV08	959888	1075	220 - 399	3762	Thr-14 to Gln-20,	H0038: 2		

HTEGV60	822954	1076	80 - 418	3763	Cys-23 to Glu-31. Tyr-12 to Phe-17, Pro-32 to Asp-39.	H0038: 1 and H0616: 1.		
HTEGV84	870240	1077	234 - 449	3764		L0758: 8, H0038: 3, H0618: 2, H0616: 2 and H0253: 1.		
HTEGW41	573880	1078	1 - 243	3765	Ser-24 to Gln-30, Asn-38 to Leu-44, Pro-46 to Glu-59.	H0038: 2	20q13.2-q13.3	118504, 118504, 131242, 139320, 139320, 139320, 139320, 139320, 602025, 602235
HTEGW94	794350	1079	1 - 351	3766	Gly-1 to Ile-7, Pro-76 to Ala-82, Asn-86 to Ile-91.	H0038: 3 and H0616: 2.		
HTEGX74	783829	1080	200 - 556	3767	Asn-1 to Asp-9, Pro-17 to Cys-23.	L0758: 5, H0038: 3, H0618: 1, H0616: 1, L0768: 1 and L0794: 1.		
HTEGY01	917214	1081	2 - 388	3768	Arg-87 to Tyr-92.	H0038: 1 and H0616: 1.		
HTEGY85	573849	1082	91 - 312	3769		H0038: 2		
HTEHB07	870707	1083	90 - 350	3770	Gly-23 to Lys-29.	H0038: 5		
HTEHC20	526704	1084	198 - 326	3771		H0038: 3		
HTEHC47	973071	1085	719 - 84	3772	Ser-32 to Thr-37, Ser-161 to Cys-167.	AR050: 13, AR051: 13, AR061: 3, AR054: 1, AR089: 1 L0758: 5, H0616: 2		

HTEHC60	965998	1086	74 - 358	3773	Thr-44 to Ala-49, Pro-60 to Arg-67, Asp-83 to Lys-95.	and H0038: 1. H0616: 3 and H0038: 2.		
HTEHC78	573882	1087	2 - 256	3774	Ala-1 to Leu-9, Thr-11 to Gly-19, Arg-31 to Thr-39, Gln-44 to Ser-58.	H0038: 2		
HTEHE60	795264	1088	2 - 223	3775	Glu-57 to Pro-63.	H0038: 1 and H0616: 1.		
HTEHE67	784926	1089	143 - 652	3776	Ala-2 to Asn-7, Glu-47 to Ile-62, Pro-71 to Trp-81, Gly-83 to Glu-88.	H0616: 2, H0038: 1 and L0794: 1.		
HTEHE78	932312	1090	194 - 301	3777	Ser-1 to Arg-6, Gly-16 to Glu-26.	H0038: 3 and L0519: 1.		
HTEHE91	790342	1091	3 - 329	3778	Gln-1 to Asp-17, Ser-51 to Arg-63, Pro-70 to Asp-78, Val-86 to Asn-93, Pro-100 to Asp-105.	H0038: 2		
HTEHF13	667224	1092	201 - 332	3779		H0038: 2 and H0616: 1.		
HTEHF66	836999	1093	2 - 436	3780	Ala-1 to Tyr-6, Ala-88 to Asp-95.	H0038: 4		
HTEHG44	933624	1094	57 - 695	3781		H0618: 1, L0023: 1, H0038: 1, H0616: 1 and L0758: 1.		
HTEHI06	935984	1095	262 - 534	3782	His-16 to Ser-22, Ala-77 to Glu-83.	L0758: 3, H0038: 2 and L0747: 1.		

HTEHI14	526687	1096	216 - 458	3783			AR089: 5, AR061: 5 H0038: 4		
HTEHI54	533960	1097	3 - 350	3784	Arg-1 to Gly-9, Pro-50 to Ala-56.		H0038: 2		
HTEHI62	922559	1098	1 - 282	3785			H0038: 2 and H0616: 1.		
HTEHI93	870629	1099	1 - 330	3786	Lys-9 to Pro-14.		H0038: 3		
HTEHJ64	530749	1100	136 - 249	3787			H0038: 2		
HTEHK40	660875	1101	2 - 301	3788	Thr-16 to Met-39.		H0038: 4		
HTEHK70	771432	1102	2 - 274	3789			H0038: 2		
HTEHK81	573866	1103	73 - 231	3790	Gln-2 to Leu-8, Asp-42 to Gly-47.		H0038: 2		
HTEHL96	573859	1104	3 - 404	3791	Glu-17 to Trp-27, Leu-29 to Phe-34, Leu-56 to Arg-61, Asn-74 to Gly-83.		H0038: 2		
HTEHO56	787521	1105	63 - 677	3792	Pro-9 to Asp-16, Gln-30 to Gln-36, Pro-69 to Ile-74, Val-78 to Pro-87, Ala-99 to Lys-112, Lys-117 to Gly-124, Lys-130 to Val-147, Ala-151 to Phe-156, Lys-180 to Asp-186.	H0616: 2, H0038: 1 and T0069: 1.			
HTEHP02	920625	1106	66 - 215	3793	Glu-13 to Pro-27, Leu-30 to Arg-37.		H0038: 2 and H0616: 2.		
HTEHP20	967443	1107	37 - 285	3794	Lys-5 to Glu-14, Arg-53 to Lys-60, Met-77 to Gln-83.		L0758: 3, H0038: 2, H0616: 2 and L0794: 1.		

HTEHP50	531505	1108	7 - 126	3795	Arg-2 to Arg-17.	H0038: 3	
HTEHP60	573853	1109	210 - 434	3796	Glu-18 to Ser-26.	H0038: 2	
HTEHP67	751866	1110	1 - 135	3797		H0616: 2, H0038: 1 and L0758: 1.	
HTEHP80	573830	1111	3 - 320	3798	His-1 to Ser-8, Asp-15 to Gln-50, Val-54 to Ser-67, Glu-76 to Lys-86, Ala-90 to Arg-105.	H0038: 2	
HTEHR83	573841	1112	3 - 197	3799	Phe-43 to Glu-49.	H0038: 2	
HTEHS19	529280	1113	1 - 237	3800	Gly-70 to Gly-75.	AR061: 5, AR089: 2 H0038: 2	
HTEHU20	573813	1114	61 - 234	3801		H0038: 2, H0616: 2 and L0758: 2.	
HTEHU68	786378	1115	109 - 294	3802	Lys-1 to Arg-6, Glu-23 to Arg-29.	H0038: 1 and H0616: 1.	
HTEHU73	870083	1116	76 - 276	3803		H0038: 2	
HTEHV72	920610	1117	1 - 357	3804	Phe-32 to Asn-37, Phe-73 to Tyr-79.	AR061: 8, AR089: 3 L0780: 3, L0759: 3, H0038: 2, L0779: 2, H0673: 1, L0803: 1, L0804: 1, L0666: 1 and H0648: 1.	
HTEHV86	785652	1118	2 - 466	3805	Ala-1 to Gly-8, Ser-52 to Lys-58, Leu-81 to Asn-86.	H0038: 1 and H0616: 1.	
HTEHW03	924832	1119	181 - 453	3806		H0038: 2	
HTEHW21	760552	1120	2 - 163	3807		H0038: 3, L0740: 2 and L0748: 1.	

HTEHX03	924826	1121	15 - 410	3808	Pro-4 to Lys-14, Thr-17 to His-22, Glu-25 to Arg-49, Pro-78 to Gly-85, Pro-120 to Phe-126.	H0616: 3, H0038: 2 and L0758: 1.		
HTEHX32	772643	1122	3 - 215	3809	Arg-19 to Asn-24, Gly-30 to Gln-47.	L0758: 5, H0616: 3, H0038: 2, L0794: 2 and H0253: 1.		
HTEHX51	668553	1123	84 - 212	3810		H0038: 2		
HTEHX92	527167	1124	17 - 292	3811		H0038: 3		
HTEIA60	859130	1125	2 - 343	3812		H0618: 2, H0038: 1 and L0783: 1.	16q24.1	256850
HTEIA80	721831	1126	10 - 225	3813		H0038: 3		
HTEIB14	963099	1127	3 - 308	3814	Gln-1 to Ser-10, Arg-18 to Thr-27, Arg-36 to Gln-65.	AR061: 7, AR089: 4 H0038: 4, H0616: 3, L0747: 3, L0663: 2, L0758: 2, H0369: 1, H0428: 1, L0769: 1, L0542: 1, L0809: 1, L0666: 1, L0665: 1, L0743: 1, L0777: 1, L0731: 1 and S0456: 1.		
HTEIF40	958355	1128	173 - 457	3815	His-16 to Ser-21, Ser-33 to Gly-60, Asp-87 to Glu-95.	H0038: 4 and H0616: 4.		
HTEIF68	573828	1129	139 - 249	3816	Ser-5 to Ile-17.	H0038: 2		
HTEIG32	699470	1130	135 - 326	3817	Leu-41 to Arg-55.	H0038: 3		
HTEIH70	573826	1131	58 - 192	3818		H0038: 2		
HTEIJ17	520113	1132	3 - 311	3819	Thr-65 to Thr-71, Arg-92 to Glu-99.	H0038: 3 and H0616: 1.		

HTEIJ41	712520	1133	1 - 186	3820	Ser-7 to Ile-13, Arg-21 to His-26, Met-33 to Ser-49.	H0038: 1, H0616: 1 and L0731: 1.		
HTEIJ73	958241	1134	40 - 255	3821	Pro-38 to Gln-54.	H0038: 1 and H0616: 1.		
HTEIJ77	772402	1135	1 - 69	3822		H0038: 1 and H0616: 1.		
HTEIK11	967431	1136	149 - 409	3823	His-8 to Ala-24, Thr-26 to Lys-33.	H0038: 2 and H0032: 1.		
HTEIK70	530454	1137	2 - 121	3824	Thr-24 to Thr-39.	H0038: 2		
HTEIK90	789121	1138	104 - 292	3825	Thr-41 to Lys-46, Arg-57 to Trp-62.	H0038: 1 and H0616: 1.		
HTEIL07	953803	1139	42 - 443	3826	Glu-13 to Thr-27.	AR061: 1, AR089: 0 L0758: 4, L0617: 2, L0794: 2, H0253: 1, H0038: 1, H0616: 1, L0789: 1 and L0779: 1.		
HTEIL48	523681	1140	83 - 271	3827		H0038: 3		
HTEIL70	520045	1141	2 - 331	3828	Lys-15 to Lys-29, Lys-36 to Thr-42, Val-48 to Thr-55, Gln-61 to Glu-80.	H0038: 2		
HTEIL71	760551	1142	1 - 246	3829	Gly-1 to Gly-6, Leu-28 to Asn-33.	H0616: 2 and H0038: 1.		
HTEIN68	753210	1143	74 - 346	3830	Gly-1 to Gly-6, Pro-12 to Pro-17, Arg-27 to Pro-40.	H0038: 2		
HTEIN95	839884	1144	159 - 545	3831	Asn-28 to Asn-33.	H0038: 1 and H0616: 1.		

HTEIO02	920622	1145	3 - 347	3832	His-1 to Arg-11.	H0038: 2 and H0616: 1.		
HTEIO12	653244	1146	152 - 334	3833	Phe-27 to Glu-39.	H0038: 3		
HTEIO28	573803	1147	159 - 356	3834		H0038: 2		
HTEIP88	941155	1148	1 - 252	3835	Met-23 to Thr-30.	AR089: 1, AR061: 0 H0038: 2 and H0253: 1.		
HTEIP92	523892	1149	194 - 370	3836		H0038: 4		
HTEIQ74	765794	1150	232 - 462	3837	Lys-1 to Trp-10.	H0038: 1 and H0616: 1.		
HTEIR33	928058	1151	41 - 472	3838	Arg-24 to Glu-38, Arg-46 to Ser-52, Pro-74 to Glu-80, Pro-118 to Ser-126.	H0616: 5, H0038: 2 and H0253: 1.		
HTEIS65	573775	1152	300 - 458	3839	Glu-15 to Lys-29.	H0038: 2		
HTEIU75	779163	1153	305 - 547	3840		H0038: 1 and H0616: 1.		
HTEIU92	870652	1154	1 - 339	3841	Asp-5 to Arg-13, Thr-37 to Ser-45.	AR061: 3, AR089: 1 H0038: 3		
HTEIV54	922027	1155	2 - 712	3842	Ala-1 to Arg-9, Thr-14 to Trp-20, Arg-46 to His-53, Pro-58 to Glu-67, Tyr-80 to Pro-86, Ile-151 to Pro-160.	H0616: 8, L0751: 6, L0753: 6, L0776: 4, L0758: 4, H0038: 3, L0759: 2, S0222: 1, L0770: 1, L0779: 1, L0731: 1 and L0608: 1.		
HTEIV86	784657	1156	1 - 231	3843	Arg-16 to Ser-23, Cys-30 to Arg-35, Arg-51 to Arg-57, Gly-62 to Thr-68.	L0779: 2, H0038: 1 and H0616: 1.		



HTEIW27	829698	1157	124 - 423	3844		H0038: 6 and H0616: 1.		
HTEIW37	573891	1158	68 - 352	3845		H0038: 2		
HTEIX28	836011	1159	204 - 554	3846	His-33 to Gly-42.	H0038: 2, L0758: 2, L0776: 1, L0809: 1, L0438: 1, H0658: 1 and L0756: 1.		
HTEIX85	864251	1160	2 - 226	3847		H0038: 2		
HTEIY52	963536	1161	58 - 216	3848	Gly-43 to Ser-48.	H0038: 1 and H0616: 1.		
HTEIY69	577783	1162	2 - 355	3849	Pro-7 to Pro-20, Pro-33 to Leu-49.	H0038: 2		
HTEIY80	955242	1163	188 - 460	3850	Thr-7 to Glu-16, Lys-24 to Asp-34, Thr-40 to Glu-48, Leu-52 to Lys-57.	H0038: 3 and L0758: 1.		
HTEIZ76	523764	1164	144 - 386	3851	Leu-5 to Gly-13.	H0038: 3, H0616: 1 and L0758: 1.		
HTEJB20	528015	1165	115 - 348	3852		H0038: 2		
HTEJB25	530590	1166	216 - 377	3853		H0038: 2		
HTEJB81	870644	1167	3 - 269	3854	Gly-47 to Ile-53.	H0038: 2		
HTEJC28	573774	1168	167 - 304	3855	Trp-14 to Glu-21, Gly-29 to Arg-36.	H0038: 2 and H0616: 1.		
HTEJC95	772989	1169	156 - 377	3856		H0616: 2 and H0038: 1.		
HTEJE15	908360	1170	2 - 319	3857		AR061: 4, AR089: 1 L0758: 7, L0794: 4, H0038: 2 and L0791: 1.		
HTEJE50	520049	1171	2 - 424	3858	Lys-9 to Lys-23,	H0038: 2		

HTEJP45	942476	1172	122 - 643	3859	Lys-30 to Lys-35. Ser-11 to Ala-19, Glu-24 to Leu-33, Pro-37 to Pro-45.	AR089: 21, AR061: 15 H0038: 2			
HTEJG24	526278	1173	79 - 276	3860		H0038: 2			
HTEJJ43	774243	1174	148 - 384	3861		H0038: 2 and H0616: 1.			
HTEJL21	573742	1175	415 - 173	3862	Gly-1 to Leu-9, Cys-15 to Arg-26, Pro-44 to Arg-50.	L0758: 12, L0794: 6, H0038: 2, L0789: 2, L0752: 2, L0803: 1 and L0779: 1.			
HTEJM56	952255	1176	115 - 294	3863	Thr-17 to Ala-24.	H0038: 1 and H0616: 1.			
HTEJN10	958389	1177	63 - 368	3864	Thr-1 to Trp-9, Glu-12 to Arg-17, Pro-23 to Gln-40.	H0038: 2 and H0616: 1.			
HTEJN49	558383	1178	1 - 126	3865		H0038: 2			
HTEJN96	573845	1179	169 - 354	3866	Thr-13 to Asn-19.	H0038: 2			
HTEJP10	914785	1180	2 - 418	3867	His-1 to Cys-7.	H0038: 2			
HTEJP66	916481	1181	475 - 645	3868		H0038: 1 and H0616: 1.			
HTEJP71	767955	1182	1 - 534	3869	Gln-12 to Ser-20.	H0415: 1 and H0038: 1.			
HTEJT37	530596	1183	3 - 194	3870	His-1 to Ser-15, Glu-29 to Lys-46, Pro-51 to Gln-63.	H0038: 2 and L0747: 1.			
HTEJT74	676254	1184	1 - 450	3871	Pro-14 to Ser-31.	H0038: 2			
HTEJU30	573823	1185	1 - 219	3872	Lys-1 to Ser-6, Glu-22 to Ser-28,	H0038: 2 and H0616: 1.			

HTEJV62	694525	1186	23 - 337	3873	Ser-48 to Arg-56. Gly-11 to Thr-17.	H0038: 2		
HTEJX78	806395	1187	2 - 388	3874	Glu-2 to Thr-11, Asn-35 to Gly-41, Thr-57 to Asn-63, Pro-73 to Glu-88, Pro-101 to Phe-110.	H0038: 2		
HTEJY21	530156	1188	3 - 440	3875	Pro-9 to Trp-16, Trp-18 to Gly-25.	H0616: 3, H0038: 2 and H0658: 1.		
HTEJY27	685272	1189	1 - 252	3876	Arg-3 to Ala-10, Asp-25 to Trp-31.	L0758: 4, L0779: 3 and H0038: 2.		
HTEJZ26	523818	1190	2 - 121	3877	Ala-1 to Pro-7, Arg-13 to Ser-22.	H0038: 2 and H0616: 1.		
HTEKC07	920925	1191	76 - 402	3878	Arg-1 to Pro-12, Trp-42 to Thr-47.	H0038: 2		
HTEKC12	815975	1192	1 - 291	3879	Gly-1 to Trp-6, Pro-12 to Ser-20.	H0038: 2		
HTEKD04	519938	1193	147 - 338	3880	Arg-7 to Ser-12, Trp-36 to Pro-60.	H0038: 5		
HTEKE41	974044	1194	103 - 315	3881	Glu-29 to Ser-36, Cys-49 to Thr-71.	H0616: 2 and H0038: 1.		
HTEKE46	870084	1195	753 - 1043	3882	Pro-22 to His-28.	H0038: 2 and H0618: 1.		
HTEKE80	790381	1196	130 - 438	3883	Glu-19 to Tyr-36, Glu-48 to Lys-53.	H0616: 3 and H0038: 2.		
HTEKF04	774260	1197	1 - 594	3884	Phe-1 to Gly-19, Gln-21 to Glu-31, Arg-79 to Lys-92, Ser-135 to Leu-145.	L0758: 5, H0616: 3 and H0038: 2.		

HTEKF24	573750	1198	103 - 267	3885	Arg-43 to Phe-48.	H0038: 2	1p13	102770, 188540, 600234, 601414, 601691, 601691, 601691, 601691, 601718, 602094
HTEKF35	573749	1199	27 - 233	3886	Pro-28 to Gly-33, Asp-35 to Leu-51, Leu-61 to Thr-69.	H0038: 2		
HTEKF68	772997	1200	1 - 291	3887	Glu-12 to Glu-19.	H0038: 2 and H0616: 1.		
HTEKI01	917176	1201	3 - 344	3888		H0038: 2		
HTEKI70	503039	1202	257 - 682	3889	Ala-24 to Tyr-31, Gln-38 to Lys-43.	H0038: 3, L0758: 2, H0253: 1, H0616: 1, L0794: 1, L0803: 1, L0745: 1 and L0588: 1.		
HTEKJ48	530588	1203	2 - 247	3890	Pro-7 to Gln-16, Arg-19 to Gly-32, Pro-34 to Glu-45, Phe-56 to Leu-65.	H0038: 2		
HTEKM14	745257	1204	1 - 264	3891	Lys-34 to Ala-42.	H0038: 3 and H0616: 1.		
HTEKO49	723148	1205	3 - 251	3892	Pro-8 to Thr-14.	H0038: 1 and H0616: 1.		
HTEKQ26	870627	1206	31 - 165	3893		H0038: 2		
HTEKQ85	784444	1207	348 - 569	3894	Lys-62 to Ser-67.	H0038: 1 and H0616:		

HTEKR75	870555	1208	139 - 318	3895		1.	H0038: 1 and H0616:		
HTEKS15	529273	1209	290 - 427	3896		1.	H0038: 2		
HTEKS20	846714	1210	3 - 569	3897			AR061: 2, AR089: 1 L0758: 14, H0038: 5, L0779: 4, L0794: 2 and H0616: 1.		
HTEKS21	506651	1211	113 - 346	3898			Pro-9 to Arg-14, Phe-34 to Ile-39, Arg-41 to Lys-47, Leu-49 to Gly-55, Lys-104 to Lys-110, Asp-119 to Gly-124.		
HTEKS76	767658	1212	166 - 399	3899			Val-1 to Val-8, Arg-36 to Pro-41, Thr-50 to Leu-55.		
HTEKX06	935945	1213	87 - 263	3900			Ser-9 to Ser-17, Leu-48 to Cys-54. Gly-46 to Glu-58.		
HTEKX08	959876	1214	118 - 375	3901			Glu-37 to Asp-46.		
HTEKX28	920927	1215	108 - 257	3902			L0758: 10, H0038: 3, L0794: 2, H0618: 1, H0253: 1 and H0616: 1.		
HTEKX70	573700	1216	68 - 259	3903			H0038: 2 and L0758:		
HTEKZ50	524054	1217	98 - 280	3904			1. H0038: 2		
HTELA50	774268	1218	49 - 195	3905			H0038: 2		
HTELD47	934272	1219	165 - 536	3906			Ile-9 to Asn-20, Ala-22 to Asp-29. Lys-8 to Lys-14.		
							H0616: 4, L0803: 1 and L0731: 1.		
							H0616: 3 and L0519:		
							2.		

HTELD82	779315	1220	79 - 267	3907	Arg-1 to Ser-6.	H0616: 2	
HTELE10	963563	1221	157 - 438	3908		H0616: 3	
HTELE41	791743	1222	260 - 475	3909	Ala-8 to Ser-13.	H0616: 5	
HTELG47	757740	1223	279 - 455	3910	Pro-2 to Asp-7.	H0038: 1 and H0616: 1.	
HTELG57	870621	1224	1 - 318	3911	Val-17 to Val-23, Phe-34 to Tyr-46, Thr-62 to His-67.	H0616: 2 and H0038: 1.	
HTELG80	773018	1225	3 - 107	3912	Val-1 to Thr-12.	H0616: 2	
HTELH44	766462	1226	351 - 542	3913	Gln-9 to His-21.	H0038: 1, H0616: 1 and L0745: 1.	
HTELI03	923071	1227	421 - 588	3914	Glu-27 to Thr-34.	H0038: 1 and H0616: 1.	
HTELI51	806403	1228	318 - 554	3915		H0616: 2 and L0749: 1.	
HTELJ89	966134	1229	86 - 361	3916	Asn-1 to Gln-7, Phe-27 to Gly-38, Pro-61 to Gly-68.	H0616: 4 and L0758: 3.	
HTELK14	794339	1230	3 - 449	3917		H0038: 1 and H0616: 1.	
HTELK50	870552	1231	9 - 239	3918	Arg-21 to Phe-28.	H0616: 2	
HTELK68	923055	1232	107 - 349	3919		H0616: 2	
HTELL48	783824	1233	181 - 294	3920		H0616: 4	
HTELL51	952267	1234	394 - 648	3921		H0616: 2	
HTELL90	952269	1235	357 - 626	3922	Asn-56 to Ser-66.	H0616: 3 and L0779: 1.	
HTELM89	786268	1236	75 - 302	3923	Asp-19 to Lys-24.	H0038: 2 and H0616: 1.	18
HTELO20	926910	1237	117 - 434	3924	Leu-21 to Gly-26,	H0616: 11 and H0038: 1.	

HTELO51	931120	1238	2 - 166	3925	His-101 to Trp-106. Ser-21 to Ser-29, Ala-43 to Asn-49.	1. H0616: 4		
HTELO73	761806	1239	56 - 232	3926	Lys-1 to Cys-7, Lys-16 to Glu-21, Ser-23 to Thr-37, Pro-40 to Ser-47, Glu-49 to Arg-59.	H0038: 1 and H0616: 1.		
HTELO93	934344	1240	1 - 204	3927	Asn-6 to Ser-12.	H0616: 2		
HTELP27	921621	1241	3 - 470	3928	Pro-1 to Val-16, Lys-22 to Asp-30, Asn-47 to Ala-61, Arg-89 to Leu-94.	H0616: 2, H0038: 1 and L0754: 1.		
HTELQ41	922634	1242	97 - 462	3929		H0616: 3		
HTELQ87	761768	1243	36 - 344	3930	Tyr-1 to Leu-7, Phe-51 to Asp-60.	H0616: 2 and H0038: 1.		
HTELR90	826531	1244	2 - 451	3931	Arg-29 to Leu-40, Gly-50 to Gln-55, Thr-73 to Ile-83, Lys-90 to Lys-95.	H0616: 2		
HTELT72	761598	1245	2 - 235	3932	Thr-7 to Asn-12, Leu-20 to Ile-29, Ser-54 to Ser-64, Met-66 to Gly-77.	H0616: 4, L0774: 2, H0618: 1, L0665: 1 and L0747: 1.		
HTELT83	780619	1246	3 - 521	3933	Lys-50 to Glu-55.	H0616: 4		
HTELU01	915339	1247	3 - 173	3934	Lys-1 to Lys-9.	H0616: 2		
HTELV06	934302	1248	37 - 240	3935	Lys-57 to Gly-63.	H0616: 2 and L0758: 1.		
HTELV10	963576	1249	106 - 270	3936	Asp-1 to Trp-11,	H0616: 2		

HTELV26	796832	1250	172 - 303	3937	Ser-49 to Lys-55. Thr-17 to Leu-22.	L0758: 16, H0038: 1 and H0616: 1.		
HTELV43	870615	1251	2 - 448	3938	Gly-2 to Ile-19, Lys-22 to Ala-31, Asp-49 to Asn-56.	H0038: 1 and H0616: 1.		
HTELV86	910946	1252	1 - 927	3939	Thr-5 to Ser-11, Asp-78 to His-85, Ser-153 to Ser-162, Glu-221 to Ala-234, Gly-247 to Glu-252.	AR089: 7, AR061: 6 H0616: 4, H0038: 1, L0745: 1 and L0779: 1.		
HTELW29	952241	1253	3 - 293	3940	Ala-21 to Trp-26, Arg-64 to Val-83.	H0616: 4, H0038: 2, L0768: 1 and L0779: 1.		
HTELW62	870596	1254	71 - 271	3941	Cys-2 to Glu-9.	H0616: 2 and L0758: 1.		
HTELX52	963506	1255	3 - 302	3942	Gln-3 to Gln-13.	H0616: 2		
HTELX72	761599	1256	25 - 117	3943		H0038: 1 and H0616: 1.		
HTELY64	764834	1257	140 - 283	3944	Thr-18 to Gly-25.	H0616: 2		
HTELZ07	952268	1258	94 - 312	3945	Lys-32 to His-41.	H0038: 1 and H0616: 1.		
HTELZ89	786424	1259	171 - 353	3946	Ser-46 to Thr-53.	H0616: 2		
HTEMA54	911666	1260	22 - 1167	3947	Gly-23 to Asn-30, Arg-45 to Lys-50.	AR089: 19, AR061: 13 9q31 H0618: 14, H0253: 12, H0038: 11, H0616: 2, L0794: 1, L0779: 1 and L0758: 1.	109400, 132800, 132800, 186855, 223900, 253800, 253800, 278700,	



HTEMB26	827055	1261	75 - 143	3948	Thr-6 to Lys-23.	H0616: 2	602088
HTEMB28	870614	1262	103 - 342	3949	Tyr-4 to Tyr-11, Ala-20 to Ser-28, Val-44 to Arg-54.	H0616: 3	
HTEMB34	870589	1263	141 - 371	3950	Leu-25 to Asn-32, Ala-49 to Phe-56, Arg-60 to Lys-69.	H0616: 3	
HTEMB72	761602	1264	1 - 306	3951		H0038: 1 and H0616: 1.	
HTEMB83	775593	1265	2 - 292	3952	Lys-49 to Lys-56.	L0758: 9, L0794: 3, H0038: 2, H0616: 2, L0790: 1 and L0779: 1.	
HTEMC18	924727	1266	1 - 453	3953	Gln-16 to Gly-27, Glu-59 to Gly-65, Ser-107 to Arg-113.	H0253: 3, H0618: 2 and H0616: 1.	
HTEMC75	848193	1267	58 - 240	3954	Gln-15 to Arg-21.	H0038: 1 and H0616: 1.	
HTEMD10	963546	1268	1 - 270	3955	Gly-1 to Glu-8, Glu-16 to Ser-22, Asp-43 to Gly-49, His-65 to Met-70, Lys-79 to Gln-90.	H0616: 2 and L0758: 2.	
HTEMD73	761783	1269	2 - 310	3956	Ala-20 to Thr-44.	H0038: 2 and H0616: 2.	
HTEMF08	958386	1270	3 - 116	3957		H0616: 2	
HTEMJ34	786377	1271	248 - 496	3958		H0616: 6 and L0758: 1.	
HTEMJ54	963531	1272	388 - 570	3959		H0616: 4, H0038: 1	

HTEMK03	923066	1273	45 - 359	3960	Pro-11 to Gly-21, Pro-65 to Ser-71.	and L0748: 1. H0038: 1 and H0616: 1.		
HTEMM80	888686	1274	353 - 631	3961	Pro-32 to Gly-40, His-54 to Glu-74.	H0616: 5, H0038: 2, L0779: 1 and L0758: 1.		
HTEMN08	958374	1275	10 - 96	3962	Tyr-16 to Ser-25.	H0616: 2		
HTEMN95	789113	1276	54 - 251	3963		H0038: 1 and H0616: 1.		
HTEMO14	880634	1277	2 - 319	3964		H0616: 2 and H0038: 1.		
HTEMO85	771434	1278	166 - 276	3965	Phe-7 to Glu-12, Leu-22 to Tyr-28.	H0616: 3		
HTEMP48	767863	1279	1 - 159	3966	Gln-29 to Gly-34.	H0616: 3 and H0038: 1.		
HTEMP49	932319	1280	3 - 629	3967	Arg-8 to Ser-15, Ser-21 to Trp-40, Glu-63 to Trp-74, Ser-76 to Ser-81, Asp-83 to Asp-96, Glu-125 to Ser-131, Leu-198 to Leu-206.	H0038: 10, L0758: 7, L0768: 6, H0253: 4, H0616: 2, L0772: 1, L0773: 1, L0779: 1 and L0731: 1.		
HTEMR65	909280	1281	2 - 340	3968	Ser-7 to Asp-13, Leu-49 to Asn-54, His-62 to Tyr-68.	AR089: 17, AR061: 13 L0794: 2, L0752: 2, H0616: 1, L0763: 1, L0766: 1, L0664: 1, H0670: 1 and L0758: 1.		
HTEMS10	963527	1282	102 - 371	3969	Arg-1 to Arg-8, Leu-44 to Ala-50, Ser-58 to Ile-68.	H0038: 1, H0616: 1 and L0758: 1.		
HTEMS48	832506	1283	45 - 203	3970	Ser-16 to His-24.	H0038: 1 and H0616:		

HTEMT06	934338	1284	2 - 268	3971	Ile-14 to Asp-22, Pro-28 to Gln-43, Pro-49 to Arg-56, Pro-62 to Ser-78, Thr-81 to Glu-89.	1. L0758: 4, H0038: 1, H0616: 1 and L0779: 1.		
HTEMT89	922999	1285	2 - 160	3972	Glu-36 to Val-53.	2. L0758: 3 and H0616:		
HTEMU17	789623	1286	112 - 273	3973	Arg-21 to Pro-26.	H0616: 2, L0749: 2 and H0038: 1.		
HTEMU54	870618	1287	43 - 189	3974	Arg-18 to Lys-24, Thr-29 to Ile-34.	H0616: 3		
HTEMX92	913795	1288	23 - 514	3975	Gly-82 to Lys-89.	AR061: 6, AR089: 3 H0616: 2 and H0038:		
HTEMY30	870662	1289	46 - 231	3976	Arg-32 to Gly-37.	1. H0038: 1, H0616: 1 and L0759: 1.		
HTEMZ04	927021	1290	162 - 377	3977		H0616: 2		
HTENA22	870601	1291	1 - 294	3978	Pro-20 to Ala-32, Arg-46 to Val-51.	H0038: 1 and H0616:		
HTENB03	923050	1292	24 - 338	3979	Ser-29 to Val-39.	1. H0616: 3		
HTENC22	775544	1293	243 - 497	3980	Gln-29 to Leu-34, Arg-36 to Leu-44, Glu-58 to Ser-64, Ser-67 to Pro-85.	H0616: 2 and L0109:		
HTENF08	958378	1294	380 - 574	3981	Ala-6 to Ala-12.	1. H0038: 1 and H0616:		
HTENF95	795316	1295	111 - 347	3982	Glu-69 to Leu-79.	1. H0038: 1, H0616: 1 and S0152: 1.		

HTENG66	840151	1296	3 - 308	3983	Asn-2 to Glu-14, Pro-17 to Lys-27, Gly-42 to Ser-59, Cys-70 to Lys-81.	H0253: 3, H0038: 1 and H0616: 1.		
HTENG93	967432	1297	1 - 102	3984	His-7 to Ser-12.	H0038: 1 and H0616: 1.		
HTENH86	784798	1298	182 - 436	3985	Ile-28 to Ser-36.	H0616: 2, H0038: 1 and L0758: 1.		
HTENI58	917213	1299	41 - 589	3986	Asn-17 to Asn-30, Glu-37 to Lys-56, Asp-64 to Gln-69, Gly-77 to Ser-95, Lys-109 to Asn-114, Arg-158 to Ser-183.	AR089: 30, AR061: 13 L0794: 25, L0758: 4, H0038: 3, H0616: 2, L0779: 2, L0768: 1 and L0790: 1.		
HTENI28	968135	1300	1 - 948	3987	Thr-6 to Arg-17.	H0038: 7, H0124: 1, H0040: 1, H0616: 1 and L0779: 1.		
HTENI76	767838	1301	3 - 443	3988	Thr-17 to Ala-25, Pro-40 to Glu-46, Asn-76 to Glu-81, Gln-90 to Lys-104.	H0253: 1 and H0616: 1.	11q13.2-q13.3 133780, 151400, 602078	
HTENK06	835851	1302	249 - 566	3989	Gly-23 to Pro-32.	H0616: 3 and H0618: 1.		
HTENK69	844557	1303	192 - 509	3990	Arg-15 to Leu-21, Ala-29 to Glu-34, Pro-40 to Trp-49, Ser-82 to Ala-97.	H0038: 4, H0616: 3, L0758: 3 and L0779: 1.		
HTENO12	917032	1304	76 - 1467	3991	Gly-29 to Glu-39, Gly-105 to Lys-117, Gln-135 to Leu-142,	H0616: 6, H0618: 3, H0253: 3 and H0038: 3.		

							Pro-180 to Ser-186, Gln-202 to Ser-207, Gln-214 to Asp-220, Gly-246 to Thr-255.				
HTEN050	969213	1305	190 - 618	3992			Asn-1 to Glu-6, Gln-9 to Gly-15, Gln-18 to Arg-40.			H0038: 1 and H0616: 1.	
HTENP54	787535	1306	17 - 208	3993			Arg-13 to Leu-18.			H0616: 17 and L0758: 1.	
HTENP80	775387	1307	2 - 496	3994			Asp-16 to Leu-22, Met-37 to Thr-42, Glu-55 to Gly-68.			H0038: 1 and H0616: 1.	
HTENQ05	928244	1308	1 - 654	3995			His-23 to Ser-34, His-77 to Glu-82.			H0038: 2, H0616: 1 and L0758: 1.	
HTENR10	963530	1309	24 - 380	3996			Gly-40 to Ala-45, Arg-65 to Thr-75.			H0038: 1 and H0616: 1.	
HTENR74	764828	1310	1 - 456	3997			Gly-1 to Pro-15.			H0038: 2 and H0616: 1.	
HTENR93	920834	1311	201 - 659	3998			Glu-49 to Ala-55, Cys-57 to Ser-85, Ser-90 to Glu-97, Ile-108 to Lys-114, Val-117 to Asn-127.			H0328: 1, H0038: 1 and H0616: 1.	
HTENS22	785996	1312	3 - 440	3999			Met-2 to Asn-16, Gln-30 to Gln-35, Met-42 to Gln-48, Ser-54 to His-60, Pro-63 to Ser-69, Leu-101 to Gln-118, Gly-139 to Pro-146.			H0038: 1, H0616: 1 and L0748: 1.	

HTENS43	784936	1313	226 - 756	4000			H0616: 5, H0038: 3, H0253: 1, L0769: 1, L0794: 1, H0521: 1, L0748: 1, L0779: 1 and L0758: 1.		
HTENS91	870515	1314	387 - 725	4001	Trp-1 to Gln-10.		H0616: 2 and L0517: 1.		
HTENV57	944416	1315	99 - 617	4002	Gly-5 to Arg-10, Arg-18 to Ser-24, Glu-35 to Asn-42, Lys-72 to Gln-82, Tyr-90 to Lys-96, Lys-112 to Arg-123, Asp-141 to Met-146.		AR061: 7, AR089: 3 H0616: 5 and H0038: 1.		
HTENW53	907717	1316	1 - 243	4003	Arg-6 to Asp-13, Lys-70 to Trp-76.		H0038: 2, H0616: 2 and L0758: 2.		
HTENX77	771409	1317	168 - 359	4004	Glu-1 to Lys-11.		L0758: 10, L0439: 6, H0616: 2, L0803: 2, L0756: 2, L0455: 1, H0038: 1 and L0438: 1.		
HTENY21	870587	1318	383 - 553	4005	Ala-17 to Ser-22.		H0038: 1 and H0616: 1.		
HTENY35	884043	1319	2 - 1009	4006	Gln-1 to Ser-19, Glu-29 to Lys-35, Leu-58 to Phe-68, Cys-100 to Arg-107, Cys-113 to Cys-119, Phe-124 to Asn-139, Leu-157 to Glu-163, Ile-174 to Ile-180.		H0616: 3		

HTENZ16	917185	1320	203 - 454	4007	Pro-195 to Pro-204, Gly-228 to Glu-250, Ile-260 to Asp-266, Thr-273 to His-279, Cys-281 to Gly-291.	L0779: 9, L0758: 9, L0665: 8, H0616: 4, L0663: 4, H0038: 3, L0755: 3, L0717: 1, L0768: 1, L0666: 1, H0659: 1, H0670: 1, L0748: 1 and L0749: 1.			
HTENZ33	870591	1321	102 - 377	4008	Gln-24 to Glu-34, Ala-58 to Ser-64.	H0038: 1 and H0616: 1.			
HTENZ72	773024	1322	2 - 400	4009	Met-56 to Pro-67, Ser-82 to Tyr-87, Pro-111 to Ala-121.	H0616: 2 and H0038: 1.			
HTEOA90	787516	1323	24 - 329	4010	Arg-20 to Gln-27, Arg-37 to His-42, Pro-46 to His-55.	H0038: 1 and H0616: 1.			
HTEOD34	812307	1324	129 - 428	4011	Tyr-3 to Cys-9, Thr-20 to Ile-25, Gly-60 to Arg-67.	H0616: 2 and H0038: 1.			
HTEOE61	918635	1325	247 - 411	4012		H0616: 2 and H0038: 1.			
HTEOF31	793202	1326	258 - 632	4013	Gly-2 to Glu-13, Val-40 to Cys-79.	H0038: 1 and H0616: 1.			
HTEOF80	847224	1327	2 - 262	4014	Val-17 to Arg-23, Tyr-28 to Ser-34, Thr-41 to Cys-47.	AR061: 7, AR089: 3 H0616: 3	Xp22	300000, 300066, 300077,	

									300310, 301220, 302350, 304050, 304110, 306100, 309530, 309585, 312040
HTEOF85	768583	1328	113 - 364	4015				H0663: 1, H0644: 1, H0038: 1 and H0616: 1. H0616: 2	
HTEOF91	918571	1329	27 - 164	4016	Arg-31 to Asp-37.				
HTEOI36	870575	1330	3 - 410	4017	Pro-17 to Ala-25, Lys-33 to Arg-40, Arg-62 to Lys-68, Ala-79 to Val-93, Lys-106 to Asp-113.			AR089: 36, AR061: 21 H0038: 7, H0618: 1, H0253: 1 and H0616: 1.	
HTEOI53	810333	1331	11 - 295	4018	Arg-1 to Ile-8, Tyr-12 to Gly-29, Lys-34 to Ala-64, Lys-77 to Glu-91.			H0038: 1 and H0616: 1.	
HTEOK02	918590	1332	121 - 408	4019				H0616: 2 and H0038: 1.	
HTEON29	815852	1333	2 - 520	4020	Pro-27 to Ala-35.			AR061: 6, AR089: 3 H0038: 4, L0758: 3, H0616: 2, L0794: 2, L0747: 2, L0803: 1, L0789: 1 and L0590: 1.	
HTEON67	954114	1334	107 - 271	4021				H0038: 2 and H0616: 1.	



HTEOU45	915138	1335	320 - 529	4022			H0616: 22		
HTEOV90	870532	1336	22 - 438	4023	Pro-14 to Phe-23, Lys-111 to Lys-133.		L0766: 5, L0803: 3, H0616: 2, L0777: 2, L0470: 1, L0761: 1, L0764: 1, L0804: 1, L0805: 1, L0776: 1, L0789: 1 and L0750: 1.		
HTEOW02	918475	1337	3 - 266	4024	Ser-30 to His-36, Arg-54 to Arg-59.		H0616: 2		
HTEOW39	870566	1338	2 - 445	4025	Gly-38 to Val-44.		AR089: 17, AR061: 14 H0616: 2		
HTEOW85	969682	1339	2 - 490	4026	Arg-1 to Ala-13, Arg-99 to Arg-104, Thr-117 to Gln-124, Asn-132 to Gln-137, Thr-145 to His-155.		H0618: 3, H0616: 2 and H0253: 1.		
HTEPA08	958391	1340	147 - 605	4027	Tyr-34 to Glu-43.		L0758: 9, H0038: 1, H0616: 1 and S0042: 1.		
HTEPA27	872923	1341	43 - 393	4028	Pro-77 to Ser-83.		H0616: 3, L0747: 2, L0794: 1, L0803: 1 and L0779: 1.		
HTEPB66	772949	1342	204 - 515	4029	Asp-35 to Gly-40.		H0616: 3, L0758: 2, L0794: 1 and L0366: 1.		
HTEPB84	782248	1343	161 - 568	4030	Leu-2 to Gly-11.		H0616: 2 and H0038: 1.		
HTEPC76	767824	1344	140 - 328	4031	Pro-10 to Asn-16, Asn-38 to Arg-44.		H0616: 4, L0779: 1 and L0758: 1.		
HTEPC87	883021	1345	126 - 497	4032	Cys-5 to Thr-14.		H0616: 2		
HTEPD06	933299	1346	2 - 193	4033	His-7 to Gly-17, Gly-25 to Leu-36.		H0616: 4, L0756: 2 and H0038: 1.		

HTEPE28	932576	1347	2 - 640	4034	Asn-30 to Lys-43, Pro-58 to Glu-65, Arg-77 to Asn-85.	AR061: 5, AR089: 2 H0369: 1, H0038: 1, H0616: 1, L0593: 1 and L0595: 1.		
HTEPG15	812303	1348	3 - 395	4035	Gln-1 to Asn-9, Pro-14 to Leu-20, Leu-42 to Gly-47, Gln-56 to Arg-61, Pro-109 to Ser-114, Lys-119 to Thr-131.	L0752: 3, H0618: 1, H0616: 1, L0769: 1, L0803: 1, L0789: 1, L0439: 1, L0758: 1 and L0698: 1.		
HTEPH01	915301	1349	25 - 477	4036	Thr-2 to Ser-12, Arg-60 to Leu-67, Ala-72 to Thr-77, Pro-82 to Lys-91, Gly-96 to Ser-101, Glu-110 to Pro-118, Gln-124 to Leu-129, Gln-132 to Ser-138.	H0616: 3 and H0038: 1.		
HTEPJ09	956200	1350	305 - 1216	4037	Arg-1 to Asn-11, His-40 to Arg-45.	H0616: 2 and L0758: 1.		
HTEPJ19	918599	1351	37 - 345	4038	Arg-1 to Ser-9.	H0616: 2		
HTEPJ79	774212	1352	27 - 122	4039		H0038: 1 and H0616: 1.		
HTEPK40	939675	1353	209 - 631	4040	Gly-5 to Pro-15, Ser-23 to His-32.	H0616: 5, L0758: 5 and H0038: 1.		
HTEPM33	870561	1354	1 - 735	4041	Pro-8 to Gly-26, Cys-54 to Cys-66, Gly-73 to His-85.	AR061: 25, AR089: 5 L0758: 3, H0616: 2, H0038: 1 and L0779: 1.		
HTEPM52	806471	1355	171 - 326	4042		H0616: 2		
HTEPN07	952243	1356	3 - 311	4043	Leu-12 to Pro-17,	H0616: 2 and H0038:		

						Pro-24 to Gly-29, Ser-34 to Gly-39. Asn-6 to Asp-16.	1.			
HTEPP23	836572	1357	1 - 192	4044				H0616: 2, L0779: 2, H0038: 1 and L0758: 1.		
HTEPP29	917207	1358	1 - 372	4045		Gly-33 to Gly-38, Gln-61 to His-66.	1.	H0038: 1 and H0616:		
HTEPP30	947107	1359	12 - 641	4046		Ala-35 to Glu-41, Ile-54 to Glu-74, Lys-80 to Leu-87.	1.	H0616: 3 and H0038:		
HTEPP32	785803	1360	3 - 866	4047		Gln-8 to Cys-17, Cys-20 to Gln-26, Thr-61 to Lys-68, His-75 to Gly-83, Asn-88 to Gln-104, Pro-118 to Leu-126, Gln-131 to Glu-138.	3.	H0616: 4 and H0038:		
HTEPP92	790869	1361	3 - 545	4048		Lys-86 to Lys-91, Lys-107 to Lys-139, Leu-155 to Asn-162.	1.	H0038: 1 and H0616:		
HTEPR90	787499	1362	1 - 168	4049			2.	H0038: 2 and H0616:		
HTEPT25	870509	1363	2 - 238	4050		Gly-42 to Gly-47.		H0616: 2		
HTEPT75	870637	1364	42 - 518	4051		Pro-66 to Ser-74.	1.	H0616: 2 and H0038:		
HTEPU01	915134	1365	533 - 670	4052				H0616: 2		
HTEPV02	917406	1366	1 - 471	4053		Ser-9 to Ser-17, Phe-21 to Leu-45.		AR061: 6, AR089: 2, H0616: 3, L0758: 2, L0768: 1, L0792: 1 and L0779: 1.		
HTEPX32	870698	1367	91 - 699	4054		Ser-10 to Gly-15,		AR089: 11, AR061: 2		

						Pro-20 to Ser-27, Glu-34 to Gly-41, Ala-45 to Trp-50, Pro-79 to Gly-88.	H0038: 6, H0616: 6, L0794: 4, L0768: 1 and L0758: 1.		
HTEPZ10	963433	1368	274 - 543	4055		Pro-9 to Ser-19, Pro-51 to Asp-57.	H0616: 2 and L0758: 2.		
HTEPZ18	888470	1369	50 - 502	4056		Lys-2 to Gly-11.	H0618: 1 and H0616: 1.		
HTEQB03	922941	1370	2 - 151	4057		Pro-30 to Cys-35, Thr-41 to Ser-47.	H0616: 4		
HTEQD40	915198	1371	2 - 490	4058		Met-11 to Lys-28.	L0758: 7, H0618: 1, H0616: 1, L0794: 1 and L0779: 1.		
HTEQD69	918579	1372	133 - 321	4059		Thr-39 to Asn-45.	H0616: 2 and H0038: 1.		
HTEQE87	958354	1373	205 - 633	4060		His-16 to Ser-21, Val-30 to Asn-40, Leu-54 to Pro-64.	H0038: 2 and H0616: 1.		
HTEQG56	881004	1374	10 - 426	4061		Pro-31 to Glu-45, Ala-52 to Lys-58, Met-78 to Lys-89.	H0616: 3 and H0038: 1.		
HTEQI54	853971	1375	189 - 422	4062		Thr-1 to Asn-6, Pro-11 to Phe-19, Arg-21 to Asn-27.	H0616: 2, L0803: 1 and L0774: 1.		
HTEQJ14	870525	1376	158 - 424	4063			H0038: 2 and H0616: 1.		
HTEQJ42	806495	1377	90 - 308	4064		Gln-4 to Ser-9, Ala-23 to Glu-29, Phe-65 to Ser-71.	H0038: 1 and H0616: 1.		
HTEQO81	806504	1378	1 - 144	4065			H0038: 1 and H0616:		

HTEQP45	966141	1379	1 - 141	4066	Lys-1 to Phe-10.	1.	H0616: 4		
HTEQQ82	932301	1380	254 - 24	4067	Asp-5 to Asp-14.	1.	H0616: 3 and L0758:		
HTEQR15	939641	1381	108 - 590	4068	Thr-17 to Leu-22.		AR089: 10, AR061: 3 H0253: 8, H0038: 4, H0616: 3, H0618: 2, L0758: 2 and L0779: 1.		
HTEQR94	966486	1382	77 - 388	4069	Asn-83 to Ser-88.		L0758: 6, H0616: 2 and L0794: 2.		
HTEQT63	924799	1383	193 - 1311	4070			L0758: 3, H0038: 1 and H0616: 1.		
HTLAB19	530577	1384	3 - 281	4071	Asp-32 to Gln-37.		H0253: 2		
HTLAB44	530579	1385	3 - 266	4072	Ala-6 to Gly-25.	3.	H0618: 4 and H0253:		
HTLAB73	575019	1386	1 - 333	4073	Gly-42 to Arg-47.		H0253: 2		
HTLAC81	679414	1387	2 - 163	4074	Leu-2 to Cys-8, Gly-32 to Arg-39.		H0253: 3		
HTLAC87	546469	1388	23 - 154	4075	Ala-1 to Arg-6, Met-14 to Thr-32.		H0038: 164, H0253: 42, H0150: 2, H0549: 1 and S0042: 1.		
HTLAD21	761758	1389	2 - 298	4076	Ser-5 to Asn-12, Leu-63 to Gly-71.		L0758: 4, H0253: 2, H0616: 2, L0649: 1, L0666: 1, L0663: 1 and L0780: 1.		
HTLAD38	421550	1390	86 - 529	4077	Phe-12 to Leu-22, Ser-26 to Tyr-32, Phe-53 to Asn-59, Tyr-68 to Leu-73,		L0758: 5, H0253: 4, L0794: 4, H0618: 2, H0038: 1, H0616: 1 and L0768: 1.		

HTLAF84	836390	1391	1 - 444	4078	Gln-96 to Gly-102. Pro-32 to Thr-48, Arg-102 to Pro-109.	H0253: 2 and L0777: 1.		
HTLAV67	530742	1392	36 - 221	4079	Ser-39 to Gly-45.	H0253: 3		
HTLBD12	506739	1393	2 - 331	4080	Ala-2 to Pro-8, Pro-57 to Trp-67, Cys-69 to Gly-74.	H0253: 2		
HTLBE55	967408	1394	2 - 232	4081	Glu-6 to Thr-15, Ser-21 to His-34, Arg-53 to Ala-64.	H0253: 1, H0038: 1 and H0616: 1.		
HTLBE82	780116	1395	209 - 481	4082	Ser-1 to Gly-8, Thr-15 to Thr-23, Pro-45 to Pro-53.	L0366: 3, H0618: 2, H0253: 1 and L0754: 1.	9q31-q34	109400, 125270, 125270, 128100, 132800, 132800, 137350, 186855, 191100, 215700, 223360, 223900, 253800, 253800, 268900, 278700, 601850, 602088
HTLBF14	971661	1396	3 - 590	4083	Glu-21 to Gln-27, Ser-30 to Lys-37.	H0616: 2, H0618: 1 and H0253: 1.		

HTLBG83	527942	1397	96 - 200	4084			H0253: 2		
HTLCA95	911655	1398	38 - 1096	4085			AR061: 373, AR089: 188 H0253: 3, H0618: 2, H0038: 2, H0616: 1 and L0758: 1.		
HTLCG77	772644	1399	2 - 112	4086		Gly-1 to Ile-6, Gly-12 to Ile-27.	L0758: 5, H0616: 3, H0038: 2, L0794: 2 and H0253: 1.		
HTLCX76	767667	1400	2 - 277	4087		Leu-58 to Arg-68.	H0253: 2		
HTLCY27	682208	1401	2 - 301	4088		Arg-9 to Cys-18, Arg-34 to Gly-40, Glu-47 to Asp-54.	H0253: 1, L0794: 1, L0766: 1, L0803: 1, H0670: 1 and L0747: 1.		
HTLCY54	908832	1402	134 - 934	4089		Arg-1 to Arg-6, Ala-49 to Tyr-58, Pro-67 to Lys-80, Ser-92 to Trp-108.	AR061: 5, AR089: 5 H0253: 4, H0618: 3, L0758: 3, L0779: 2 and L0794: 1.		
HTLCZ48	572959	1403	1 - 162	4090		His-1 to Gly-6.	H0253: 2		
HTLCZ96	815897	1404	17 - 286	4091			L0758: 4, L0794: 2, L0617: 1, H0253: 1, H0038: 1, L0789: 1 and L0779: 1.		
HTLDA58	828115	1405	2 - 271	4092		Ser-6 to Ser-11.	H0253: 2		
HTLDE53	780842	1406	72 - 497	4093		Asn-1 to Glu-6, Gly-17 to His-28, Glu-33 to Ser-39, Pro-41 to Lys-51, Pro-56 to Glu-69, Ser-83 to Lys-90, Thr-97 to Ser-103,	L0758: 11, H0253: 3, H0550: 1 and H0616: 1.		

HTLDE64	908613	1407	83 - 427	4094	Arg-121 to Asp-131. Glu-15 to Leu-20, Leu-24 to Ser-47.	AR089: 25, AR061: 11 H0253: 2 and H0618: 1.			
HTLDE95	616724	1408	86 - 298	4095		H0253: 2			
HTLDF33	909254	1409	3 - 599	4096	Pro-7 to Gly-13.	AR061: 7, AR089: 3 L0758: 6, L0789: 2, L0779: 2, H0253: 1, L0809: 1, L0666: 1 and H0648: 1.			
HTLDG55	911645	1410	1 - 192	4097	Gly-1 to Arg-10.	H0253: 2			
HTLDH65	839795	1411	3 - 431	4098		H0553: 3 and H0253: 1.			
HTLDI90	835850	1412	248 - 472	4099		H0618: 1 and H0253: 1.			
HTLDO94	915223	1413	90 - 458	4100	Met-12 to Asp-18, Tyr-20 to Gly-31, Lys-38 to Trp-47.	H0253: 2, H0188: 1 and H0038: 1.			
HTLDP77	920546	1414	1 - 573	4101	Gly-1 to Gly-9, Gln-15 to Arg-20, Cys-53 to Arg-59, Arg-84 to Glu-89, Pro-105 to Glu-113.	H0253: 3 and H0618: 2.			
HTLDQ25	870057	1415	1 - 834	4102	Ser-3 to Ser-16.	H0618: 11, H0253: 10, H0616: 6, L0758: 5, H0038: 4, L0768: 2 and H0090: 1.			
HTLDS55	891322	1416	2 - 1171	4103	Ala-1 to Gln-13, Pro-19 to Leu-27, Asp-34 to Pro-40,	AR061: 7, AR089: 2, AR054: 2, AR051: 2, AR050: 2			



						Ser-45 to Ser-52, Lys-105 to Pro-112, Pro-146 to Trp-158, Arg-181 to Arg-189, Arg-241 to Arg-248, Asp-285 to Asn-291, Gln-328 to Ile-333, Gln-369 to Thr-375, Arg-380 to Phe-390.	H0618: 5, L0758: 4, H0038: 3, H0253: 2, H0553: 1, H0616: 1, L0789: 1, L0663: 1 and L0779: 1.			
HTLDT05	909752	1417	2 - 328	4104		Gly-3 to Ser-8.	AR089: 11, AR061: 7 H0253: 2, L0439: 1 and L0599: 1.			
HTLDT81	952265	1418	1 - 465	4105		Pro-3 to Pro-8, Glu-22 to Gln-29.	H0253: 2 and H0618: 1.			
HTLDU05	911649	1419	2 - 469	4106		Pro-89 to Ala-97.	AR061: 8, AR089: 7 H0253: 3, H0618: 1 and L0758: 1.	9q31	109400, 132800, 132800, 186855, 223900, 253800, 253800, 278700, 602088	
HTLDV31	867748	1420	61 - 309	4107		Gln-16 to Gly-35, Gly-59 to Ser-74.	H0253: 1 and S0152: 1.			
HTLDX88	791684	1421	148 - 636	4108		Pro-5 to Gly-10, Gly-24 to Ala-33, Pro-88 to Pro-95, Pro-106 to His-114.	H0618: 2 and H0253: 1.			
HTLDY85	573746	1422	3 - 425	4109		Lys-50 to Ala-55,	H0038: 2 and H0253:			

							Thr-99 to Glu-104, Arg-116 to Arg-122, Lys-129 to Thr-136.	1.				
HTLDZ14	573401	1423	174 - 347	4110				H0253: 2				
HTLEB14	573464	1424	1 - 414	4111			Gly-63 to Arg-71.	3.	H0618: 4 and H0253:			
HTLED72	906989	1425	102 - 287	4112			Leu-1 to Pro-7.		H0253: 2			
HTLEF94	870258	1426	33 - 239	4113					H0253: 2			
HTLEG65	870154	1427	177 - 1181	4114					AR051: 12, AR054: 10, AR050: 8 H0616: 6, H0618: 2, H0253: 2 and H0038: 2.			
HTLEG91	870257	1428	1 - 111	4115					H0253: 2			
HTLEH30	934287	1429	1 - 528	4116			Gly-1 to His-8, Glu-26 to Gly-33.		H0253: 2			
HTLEI47	573460	1430	124 - 417	4117			Glu-58 to Thr-63.		H0253: 3			
HTLEJ11	973302	1431	2 - 802	4118			Tyr-52 to Gln-60, Phe-86 to Ala-94, Lys-111 to Arg-118, His-193 to Tyr-198.		AR061: 3, AR089: 1 H0618: 3 and H0253: 1.	15q13-qter		
HTLEJ93	960314	1432	2 - 307	4119			His-22 to Lys-36, Asp-51 to Lys-59, Gln-68 to Leu-83.		H0253: 5 and H0618: 3.			
HTLEK64	506747	1433	2 - 331	4120			Ala-1 to Cys-13, Arg-32 to Ala-37.		H0253: 2			
HTLEL01	917022	1434	2 - 202	4121			Pro-3 to Gly-9.		H0253: 1 and H0616: 1.			
HTLEL03	575080	1435	2 - 106	4122					H0253: 2	3p21.3	116806, 120120,	

								120120, 120120, 120436, 120436, 120436, 138320, 168468, 182280, 600163
HTLEL07	953712	1436	58 - 555	4123	Ala-29 to Asn-37, Lys-64 to Thr-77, Ile-97 to Arg-126.	H0253: 1 and H0617: 1.		
HTLEL31	669950	1437	3 - 143	4124	Pro-6 to Glu-13, Arg-18 to Pro-30.	H0253: 2	7q22	126650, 126650, 154276, 173360, 173360, 602136, 602136, 602136, 602447
HTLEM46	719160	1438	1 - 456	4125		H0253: 2, L0777: 2 and L0759: 1.		
HTLEO50	506649	1439	2 - 265	4126	Ser-2 to Pro-10.	H0253: 1 and H0038: 1.		
HTLEP16	574942	1440	3 - 443	4127		H0253: 2, L0794: 2 and S0042: 1.		
HTLEQ07	953706	1441	3 - 605	4128	His-7 to Ile-32, Glu-82 to Glu-87, Lys-103 to Gly-108.	H0618: 2 and H0253: 1.		

HTLES43	573403	1442	49 - 216	4129		H0253: 2		
HTLES54	574884	1443	1 - 282	4130	Pro-10 to Gln-19, Pro-46 to Ile-59, Thr-64 to Leu-70.	H0038: 2 and H0253: 1.		
HTLET56	911654	1444	95 - 826	4131	Ser-54 to Lys-61, Pro-118 to Lys-128, Thr-208 to Ser-213, Ser-218 to Ala-227, Pro-230 to Ser-236, Pro-238 to Ser-244.	AR061: 6, AR089: 5 H0253: 18, H0618: 7, L0794: 3, H0038: 1, H0616: 1, L0788: 1 and L0758: 1.		
HTLET78	836820	1445	2 - 826	4132	Leu-11 to Lys-18, Phe-107 to Gly-114, Glu-121 to Asn-128, Met-146 to Pro-153.	AR061: 4, AR089: 2 H0618: 10, H0253: 5, L0758: 5, L0664: 1, L0756: 1, L0779: 1 and L0698: 1.		
HTLET93	573454	1446	1 - 111	4133		H0253: 2		
HTLEV33	527956	1447	1 - 273	4134	Ala-8 to Gly-17, Pro-25 to His-34.	L0794: 5, H0253: 3, H0618: 2, H0616: 2, L0758: 2 and L0787: 1.		
HTLEV95	883332	1448	52 - 414	4135	His-1 to Thr-6, His-14 to Cys-58, Cys-70 to Ala-77, Pro-85 to Cys-109, Pro-116 to Glu-121.	H0616: 14, H0618: 8, L0779: 4, H0253: 3, H0038: 3, L0790: 1 and L0758: 1.		
HTLEW12	870255	1449	2 - 346	4136		H0253: 2, H0617: 2 and H0618: 1.		
HTLEW21	573458	1450	3 - 197	4137		H0253: 2		
HTLEY11	967309	1451	2 - 130	4138	Arg-1 to Gly-21, Gln-38 to Asp-43.	H0253: 2		
HTLEY91	775310	1452	5 - 226	4139	Pro-38 to Trp-43,	H0253: 2		

							Pro-47 to Lys-54, Gly-62 to Arg-72.				
HTLEZ14	791662	1453	2 - 334	4140			Asn-18 to Pro-44, Val-64 to Phe-70.			H0618: 4 and H0253: 3.	
HTLEZ15	934288	1454	3 - 251	4141			Pro-5 to His-12, Glu-30 to Thr-36.			H0618: 2 and H0253: 2.	
HTLEZ32	870261	1455	3 - 209	4142						H0253: 2	
HTLFA74	934172	1456	279 - 707	4143			Ser-20 to Glu-26, Gly-31 to Ala-46, Thr-62 to His-67, Arg-72 to Pro-81.			H0253: 2 and H0618: 1.	
HTLFC20	917128	1457	409 - 1041	4144			Ala-4 to Trp-10, Glu-27 to Gln-32, Gly-115 to Gly-122.			H0618: 3 and H0253: 3.	
HTLFE01	917033	1458	98 - 313	4145			Asn-7 to Val-12, Leu-15 to Ser-23.			H0253: 4 and H0038: 1.	
HTLFE05	954984	1459	3 - 812	4146			His-1 to Cys-6, Glu-24 to Gly-29, Gln-53 to Asp-59, Gly-80 to Pro-86, Glu-142 to Ser-148, Ser-154 to Val-160, Pro-163 to Gln-180, Val-195 to Pro-200, Lys-205 to Ser-213, Ala-222 to Glu-228, Asp-239 to Gly-270.		7q22	H0253: 5, H0618: 4, H0038: 1 and H0616: 1.	126650, 126650, 154276, 173360, 173360, 602136, 602136, 602136, 602447
HTLFE20	934278	1460	80 - 475	4147			Gly-11 to Val-29, Gly-31 to Glu-38, Ala-40 to Arg-48,			H0253: 8 and H0618: 7.	

						Gly-55 to Val-65, Leu-70 to Thr-76.				
HTLFI28	775392	1461	2 - 430	4148		Pro-24 to Arg-31, Ile-66 to Leu-72, Asp-90 to Glu-98.	H0253: 3 and H0038: 2.			
HTLFI39	953730	1462	2 - 622	4149		Ala-15 to Asp-23, Thr-44 to Tyr-52.	AR089: 19, AR061: 13 H0618: 8 and H0253: 4.	7q22	126650, 126650, 154276, 173360, 173360, 602136, 602136, 602136, 602447	
HTLFI83	781303	1463	19 - 513	4150		Asp-13 to Leu-26, Val-38 to Val-76.	H0253: 1 and H0038: 1.			
HTLFI39	573462	1464	2 - 343	4151		Gln-7 to Phe-13, Leu-24 to Val-37, Pro-50 to Leu-65.	H0253: 2			
HTLGD25	870136	1465	28 - 600	4152		Gly-3 to Gly-9, Leu-51 to Gln-58, Leu-67 to Ser-74, His-100 to Pro-106, Arg-132 to Arg-138.	AR061: 3, AR089: 1 H0618: 4, H0253: 4, H0616: 2, L0758: 2 and H0038: 1.			
HTLGD69	835493	1466	287 - 652	4153		His-27 to Ser-39, His-47 to Pro-55.	L0758: 2, H0618: 1, H0253: 1, H0616: 1 and L0779: 1.			
HTLGG36	789656	1467	2 - 574	4154		Thr-13 to Ser-21, Arg-26 to His-44, Ala-85 to Cys-91.	H0618: 4, L0779: 1 and L0758: 1.			

HTLGK55	868309	1468	1 - 483	4155	Thr-104 to Thr-121, Gly-156 to Arg-163.	H0618: 2, H0617: 1 and L0743: 1.			
HTLGM02	964878	1469	62 - 766	4156	Lys-1 to Gly-12, Glu-32 to Phe-41, Arg-69 to Leu-81, Pro-188 to Ile-195.	H0618: 2			
HTLGM07	952254	1470	3 - 761	4157	Arg-1 to Glu-6, Ile-15 to Phe-23, Gly-59 to Phe-72, Pro-95 to Trp-112, Phe-117 to Pro-129.	AR089: 21, AR061: 16 H0618: 32, H0253: 13, H0616: 6, L0758: 3, H0038: 2, L0794: 2, H0009: 1, H0688: 1, L0769: 1, L0372: 1, L0646: 1, L0363: 1, L0766: 1, L0790: 1, L0665: 1, H0670: 1 and L0779: 1.			
HTLGT62	918606	1471	2 - 547	4158	Asn-4 to Thr-10, Pro-46 to Asp-51.	H0618: 9, H0253: 1 and L0758: 1.			
HTLGW17	958208	1472	1 - 768	4159	Arg-39 to Asn-44, Arg-55 to Gly-62, Arg-98 to Ile-103.	H0618: 3 and H0253: 3.			
HTLGX90	870528	1473	61 - 906	4160	Pro-41 to Gly-57, Leu-76 to Gly-83, Pro-87 to Ser-95, Glu-97 to Pro-106, Ile-122 to Glu-128, Gln-152 to Arg-166, Thr-180 to Arg-187.	L0748: 4, H0618: 3, L0751: 3, L0749: 2, L0777: 2, H0038: 1, H0616: 1, L0772: 1 and L0775: 1.			

HTLHC14	908428	1474	3 - 503	4161	Leu-191 to Pro-199, Glu-231 to Cys-241, Val-248 to Asp-255. Gly-38 to Phe-51, Pro-74 to Trp-91, Phe-96 to Ala-127, Glu-130 to Gly-148.	AR061: 7, AR089: 4 H0618: 32, H0253: 13, H0616: 6, L0758: 3, H0038: 2, L0794: 2, H0009: 1, H0688: 1, L0769: 1, L0372: 1, L0646: 1, L0363: 1, L0766: 1, L0790: 1, L0665: 1, H0670: 1 and L0779: 1.		
HTLHE72	963471	1475	62 - 508	4162		H0618: 3 and H0253: 1.		
HTLHL82	958334	1476	186 - 1103	4163	Gln-1 to Trp-27.	H0253: 11, H0618: 8, L0779: 3, L0758: 3 and L0768: 1.		
HTLHO94	968685	1477	298 - 164	4164	Lys-36 to Glu-45.	H0038: 2, L0747: 2, H0618: 1, L0665: 1, L0779: 1 and L0758: 1.		
HTLHP32	933335	1478	87 - 455	4165	Phe-6 to Ala-12, Arg-24 to Arg-35, Leu-66 to Phe-84.	AR089: 35, AR061: 7 H0618: 2		
HTLHP52	926980	1479	11 - 181	4166	Glu-37 to Gln-42.	H0618: 2		
HTLHP80	870156	1480	350 - 604	4167		H0618: 2		
HTLHT15	946586	1481	1 - 381	4168	Tyr-31 to Arg-42, Met-63 to Leu-69, Tyr-114 to His-123.	H0618: 2		
HTLHT24	870254	1482	21 - 893	4169	Pro-1 to Ala-10,	H0618: 26, H0253: 20		



						Val-27 to Gly-42, Asp-61 to Asp-66, Ser-81 to Ala-88.	and L0758: 1.		
HTLHU04	926950	1483	2 - 943	4170		Gln-10 to Ile-18, Arg-41 to Ala-59, His-115 to Lys-128, Lys-143 to Glu-151, Thr-164 to Glu-169.	L0758: 8, H0618: 4, H0253: 1, H0038: 1 and L0769: 1.		
HTLHV67	936139	1484	2 - 700	4171		Glu-2 to Thr-7, Arg-64 to Lys-72, Glu-77 to Leu-83, Arg-93 to Ser-102, Ile-118 to Gln-123.	H0618: 3	15q23-q25	118485, 151670, 231680, 272800, 272800, 272800, 276700, 600374, 601780
HTLHZ08	958321	1485	1 - 675	4172		Ser-134 to Glu-139, Thr-154 to Leu-160.	H0618: 2		
HTLHZ10	963475	1486	2 - 241	4173		Arg-1 to Gln-13, Phe-16 to Pro-62.	H0618: 1 and H0253: 1.		
HTLIA92	784817	1487	96 - 656	4174		Pro-7 to Lys-15, Asp-21 to Ser-28, Gln-53 to Ala-58, Thr-115 to Asn-127.	H0618: 2, L0764: 2, H0253: 1, L0492: 1, H0673: 1 and H0038: 1.		
HTLID36	945891	1488	1 - 417	4175		Thr-10 to Thr-18, Pro-58 to Val-65.	AR089: 7, AR061: 7 H0618: 1 and H0038: 1.		
HTLIK11	966043	1489	133 - 312	4176		Pro-11 to His-17, Pro-27 to Asp-36.	H0618: 2		

HTLIP19	958351	1490	3 - 899	4177	Ser-38 to His-43. Ser-25 to Thr-32, His-50 to Lys-56, Glu-111 to Asp-116, Trp-156 to Lys-161, Leu-189 to Arg-202, Asp-258 to Thr-264.	L0758: 6, H0616: 3, H0038: 2 and H0618: 1.		
HTLIQ09	931046	1491	501 - 644	4178	Leu-11 to Leu-17, Pro-22 to Leu-27, Pro-40 to Lys-46, Arg-66 to Pro-73, Thr-91 to Ser-98, Val-102 to Lys-108, Gly-125 to Glu-130, Leu-138 to Asp-144, Arg-149 to Arg-158.	H0618: 2 H0618: 1 and H0253: 1.		
HTLIR30	870115	1492	3 - 659	4179				
HTLIU76	946300	1493	46 - 609	4180	Pro-13 to Ala-18, His-30 to Gln-37, Gly-49 to Ala-66, Ala-80 to Lys-92, Glu-98 to Asp-103, His-119 to Thr-126.	AR089: 9, AR061: 8 L0758: 12, H0618: 6, H0038: 3, H0253: 1, H0050: 1, L0151: 1 and L0768: 1.		
HTLIV78	947234	1494	618 - 97	4181	Pro-18 to Asp-23, Arg-110 to Gln-122.	AR089: 9, AR061: 7 L0758: 10, L0794: 3, H0618: 2, H0038: 2, H0253: 1, L0768: 1 and L0789: 1.		
HTLIY52	942161	1495	1 - 1368	4182		AR061: 0, AR089: 0 H0618: 64, H0253: 52,		

HTLJA23	953729	1496	2 - 814	4183	Thr-50 to Tyr-58, Gly-155 to Gln-161, Thr-164 to Gln-175.	L0758: 6, L0779: 2, H0392: 1, H0038: 1, L0761: 1, L0803: 1, L0806: 1 and L0697: 1. H0618: 8 and H0253: 4.	7q22	126650, 126650, 154276, 173360, 173360, 602136, 602136, 602136, 602447
HTLJA24	934279	1497	3 - 572	4184	Ile-1 to Trp-9, Gly-35 to Val-53, Gly-55 to Glu-62, Ala-64 to Arg-72, Gly-79 to Arg-85.	H0618: 2		
HTLJC71	922923	1498	3 - 1355	4185	His-1 to Phe-9, Cys-13 to Thr-18, Pro-35 to Gly-48, Glu-61 to Pro-68, Lys-105 to Ala-136, Thr-144 to Gln-154, Leu-163 to Gly-171, Thr-205 to Gln-222, Pro-251 to Gln-257.	AR061: 7, AR089: 5 H0618: 12, H0253: 8, H0038: 6, L0758: 6, L0779: 5, H0616: 3, T0041: 1, L0776: 1, S0274: 1 and H0543: 1.		
HTLJD35	967336	1499	1 - 192	4186	Cys-5 to Ser-15, Pro-36 to Pro-44.	H0618: 1 and H0253: 1.		
HTLJD88	953714	1500	161 - 760	4187	Arg-15 to Glu-25,	H0253: 5 and H0618:		

HTLJJ75	924755	1501	1 - 921	4188	Lys-35 to Val-41, Gln-70 to Pro-100. Gln-1 to Thr-12.	2. AR089: 11, AR061: 9 H0253: 7, H0618: 6, L0794: 2, L0779: 2, L0595: 2, H0687: 1, L0438: 1, L0741: 1 and L0758: 1.		
HTLJL23	922994	1502	2 - 619	4189	Leu-9 to Ser-14.	H0618: 3, H0038: 3, H0616: 3 and H0253: 2.		
HTTAD55	835652	1503	132 - 245	4190		H0040: 3		
HTTAE49	723331	1504	74 - 160	4191		H0040: 2		
HTTAH87	509574	1505	2 - 232	4192		H0040: 2		
HTTAJ35	707750	1506	3 - 194	4193	Leu-10 to Lys-16, Asn-43 to Ser-49.	L0770: 3, L0766: 3, L0759: 3, L0790: 2, H0659: 2, H0040: 1, L0776: 1, L0663: 1, L0665: 1, L0752: 1 and L0755: 1.		
HTTAJ50	509657	1507	1 - 261	4194		H0040: 2		
HTTAN57	509453	1508	29 - 274	4195	Gly-21 to Gly-27, Pro-38 to Gly-49, Ser-68 to Asp-73.	H0040: 2		
HTTAS96	961057	1509	91 - 255	4196	Arg-7 to Cys-13, Ser-16 to Arg-21, Ala-28 to Gly-33.	H0040: 2		
HTTAU82	797726	1510	61 - 309	4197	Pro-6 to Asn-13, Thr-25 to Gly-34.	H0040: 2		
HTTBE25	509128	1511	1 - 156	4198		H0040: 2		

HTTBH34	530565	1512	177 - 326	4199	Pro-14 to Gly-20, Leu-23 to Asn-33.	H0040: 1, L0438: 1 and H0658: 1.		
HTTBH41	530562	1513	106 - 264	4200	Ser-16 to Lys-22, Ser-29 to Gln-35.	H0031: 1 and H0040: 1.		
HTTBH54	530563	1514	114 - 266	4201		H0040: 2		
HTTBH94	530564	1515	3 - 263	4202	Thr-3 to Arg-14.	AR061: 4, AR089: 3 H0040: 2		
HTTBN67	578085	1516	54 - 176	4203		H0040: 2		
HTTCA15	869705	1517	2 - 262	4204	Glu-74 to Tyr-79.	H0040: 2		
HTTCD03	925390	1518	248 - 391	4205	Asn-1 to Ser-13.	H0040: 2		
HTTCD71	530393	1519	3 - 101	4206		H0040: 2		
HTTCL35	529672	1520	72 - 185	4207		H0040: 2, L0766: 1 and L0758: 1.		
HTTCT34	973210	1521	3 - 1049	4208	Phe-86 to Tyr-94, Val-149 to Lys-155, Trp-169 to Asn-179, Thr-189 to Glu-197.	AR061: 5, AR089: 2 H0040: 3		
HTTDF50	526385	1522	191 - 298	4209		H0040: 2		
HTTDF90	917155	1523	78 - 260	4210		H0040: 3		
HTTDG36	968131	1524	26 - 280	4211	Gly-13 to Gly-19, Pro-38 to Gly-50, Glu-67 to Gly-73.	H0040: 2		
HTTDI21	869686	1525	3 - 188	4212		H0040: 1 and H0634: 1.		
HTTDJ65	973307	1526	155 - 364	4213	Ser-2 to Val-16, Pro-50 to Trp-56.	H0040: 3		
HTTDL38	573641	1527	47 - 136	4214		H0040: 2		
HTTDL45	523452	1528	3 - 89	4215		H0040: 3 and L0792: 1.		

HTTDL89	959837	1529	183 - 341	4216		H0040: 2	
HTTDN40	734318	1530	52 - 387	4217	Gln-8 to Ser-13, Asp-20 to Tyr-27.	H0040: 2	
HTTDN85	783444	1531	89 - 313	4218		H0040: 2	
HTTDO19	908937	1532	1 - 333	4219	Thr-3 to Lys-9, Gly-14 to His-26, His-30 to Lys-37, Lys-43 to Ser-49.	AR089: 16, AR061: 9 H0040: 2	
HTTDO37	573685	1533	150 - 440	4220	Phe-25 to Phe-38.	H0040: 2 and H0670: 1.	
HTTDR91	790336	1534	110 - 280	4221	Ile-3 to Lys-9.	H0040: 2 and L0766: 1.	
HTTDR92	573666	1535	190 - 330	4222	Gly-8 to His-21.	H0040: 2	
HTTDS02	920589	1536	217 - 387	4223		H0040: 2	
HTTDX84	921100	1537	1 - 480	4224	Pro-33 to Arg-43, Ala-48 to Tyr-57.	H0253: 3, L0758: 2, H0618: 1, H0038: 1 and H0040: 1.	
HTTDZ54	692608	1538	125 - 298	4225		H0040: 2	
HTTDZ91	523206	1539	2 - 313	4226	Ser-11 to Ala-19, Lys-27 to Ala-33.	H0618: 1 and H0040: 1.	
HTTEB33	573719	1540	227 - 349	4227		H0040: 2	
HTTEH58	747943	1541	149 - 286	4228		H0040: 2	
HTTEL50	745985	1542	102 - 209	4229		H0040: 2	
HTTEU68	967819	1543	2 - 766	4230	Lys-8 to Val-20, Ser-72 to Ala-77, Ala-84 to Ser-92, Leu-110 to Lys-119.	H0040: 2, L0439: 2, L0438: 1 and L0747: 1.	
HTTEV62	573614	1544	85 - 285	4231	Ser-1 to Gln-7, Arg-9 to Glu-14,	H0040: 2, H0616: 1, L0794: 1, L0779: 1 and	

							Pro-16 to Val-24, Arg-35 to Asp-40.	L0758: 1.			
HTTEY64	974107	1545	207 - 464	4232				H0040: 4			
HTTEY67	917903	1546	598 - 804	4233			Ala-1 to Ala-7, Gly-53 to Lys-67.	H0040: 2, H0435: 1, L0439: 1 and L0759: 1.			
HTTEZ34	771602	1547	168 - 329	4234			Arg-40 to Asn-45.	H0040: 2			
HTTFA16	870198	1548	1 - 408	4235				H0040: 1, S0150: 1 and L0601: 1.			
HTTFB60	869666	1549	2 - 220	4236				H0040: 2			
HTTFG35	778426	1550	1 - 183	4237			Asp-14 to Gln-22.	H0040: 5			
HTTFG83	974284	1551	235 - 441	4238				H0040: 2, H0169: 1 and L0753: 1.			
HTTFH70	757358	1552	139 - 285	4239				H0040: 2			
HTTFK90	787599	1553	36 - 263	4240			Arg-25 to Trp-32.	H0040: 2, L0794: 2, L0659: 1, L0809: 1, L0779: 1 and L0752: 1.			
HTTFL89	974346	1554	99 - 419	4241			Gly-15 to Gly-21, Pro-31 to Pro-46.	H0040: 3			
HTTFM17	750942	1555	52 - 219	4242				H0040: 2, L0805: 1 and L0758: 1.	17q		
HTTFM66	950051	1556	141 - 1079	4243				AR061: 6, AR089: 2 H0040: 2			
HTTFS59	825922	1557	1 - 273	4244				H0040: 2, L0748: 2, L0749: 2 and L0766: 1.	11p11.2-p11.1	133701, 168500, 171650, 176930, 176930, 600623, 600811,	

HTTFT08	934460	1558	34 - 207	4245	Asn-23 to Gln-29, Arg-37 to Asn-43.	H0040: 3	600958
HTTFV93	925544	1559	47 - 169	4246	Asp-36 to Lys-41.	H0040: 2	
HTTFW03	923105	1560	53 - 202	4247		H0615: 1 and H0040: 1.	
HTTFX21	924775	1561	63 - 212	4248		L0748: 13, L0770: 4, L0777: 3, H0040: 2, L0794: 2, L0528: 2, L0789: 2, L0758: 2, H0685: 1, H0688: 1, L0662: 1, L0768: 1, L0766: 1, L0657: 1, L0526: 1, L0809: 1, L0439: 1 and L0740: 1. H0040: 2 and H0634: 1.	
HTTFZ70	974066	1562	114 - 329	4249	Lys-20 to Lys-27.		
HTTHH05	931004	1563	436 - 606	4250	Tyr-12 to Gly-17.	H0634: 2	
HTTHU43	953479	1564	207 - 542	4251		L0755: 3, L0766: 2, H0031: 1, H0634: 1, L0439: 1 and L0759: 1.	
HTTIG04	926752	1565	2 - 235	4252	His-54 to Ser-61.	H0634: 2	
HTTIH23	869636	1566	2 - 247	4253	Lys-47 to Asp-56.	H0634: 2	
HTTIH80	869635	1567	32 - 226	4254		H0040: 1 and H0634: 1.	
HTTIL06	934089	1568	547 - 717	4255		H0040: 1, H0634: 1 and L0485: 1.	
HTTIN23	869634	1569	338 - 553	4256	Gln-15 to Thr-20.	H0634: 2	
HTTIU05	931015	1570	158 - 430	4257	Ala-17 to Gln-28,	H0634: 2	



HTTW81	922817	1571	294 - 446	4258	Pro-73 to Thr-83.	H0634: 3		
HTTZ05	930994	1572	112 - 354	4259	Ser-60 to Pro-69.	H0634: 2		
HTTJA11	839725	1573	13 - 240	4260	Glu-54 to Lys-60, Pro-65 to Gly-74.	H0040: 1, H0634: 1 and L0803: 1.		
HTTJA47	869618	1574	18 - 356	4261	Glu-61 to Lys-66, Met-76 to Asn-83.	H0040: 1 and H0634: 1.		
HTTJH13	869615	1575	3 - 182	4262	Gln-11 to Gly-17, Glu-26 to Ser-36, Arg-53 to Ala-60.	H0634: 2		
HTTJM01	913799	1576	137 - 283	4263	Pro-14 to Pro-20.	H0634: 2		
HTTJQ06	934130	1577	61 - 177	4264		H0040: 1 and H0634: 1.		
HTTJX68	974063	1578	1 - 147	4265	Arg-29 to Arg-41.	H0040: 1 and H0634: 1.		
HTTJY08	958170	1579	169 - 276	4266		H0634: 2		
HTTKD44	948750	1580	2 - 448	4267	Lys-13 to Arg-21, Gly-26 to Thr-36.	H0549: 1 and H0634: 1.		
HTTKF89	960928	1581	1 - 189	4268		H0040: 2 and H0634: 1.		
HTTKG34	915033	1582	56 - 181	4269		H0634: 2		
HTTKK06	974311	1583	210 - 383	4270		H0634: 3		
HTTKL80	974316	1584	228 - 362	4271		H0634: 3		
HTTKN21	974310	1585	354 - 509	4272		H0634: 3		
HTTKN30	920893	1586	166 - 429	4273	Asn-54 to Leu-60.	H0634: 1, H0672: 1 and L0740: 1.		
HTTKP07	911390	1587	2 - 337	4274	Thr-15 to Asp-25, Glu-69 to Leu-89.	AR089: 1, AR061: 1 H0634: 2		
HTTKS13	926795	1588	65 - 484	4275	Ala-12 to Gly-22,	H0634: 2		

HTTKV17	830008	1589	2 - 193	4276	Pro-38 to Ser-45, Ala-77 to Pro-83, Ala-88 to Gly-93.			
HUDAM29	529157	1590	3 - 224	4277	Thr-1 to Gln-7, Gly-13 to Gln-37.	H0634: 2		
HUDBZ78	739638	1591	2 - 163	4278		S0042: 2		
HUKAA62	503626	1592	308 - 81	4279	Ala-4 to Val-11, Gly-58 to Leu-64.	H0038: 1 and S0042: 1. H0059: 2		
HUKAB80	503445	1593	210 - 347	4280		H0059: 2		
HUKAC72	966804	1594	1 - 309	4281	Glu-1 to Arg-14.	H0059: 2		
HUKAM82	954420	1595	122 - 322	4282		H0059: 3		
HUKAX07	954359	1596	36 - 164	4283	Gly-23 to Pro-31.	H0059: 2		
HUKCC86	529727	1597	57 - 224	4284	Pro-1 to Lys-7.	H0059: 2		
HUKDH28	531165	1598	26 - 334	4285	Ser-27 to Thr-35.	H0059: 2		
HUKDH50	531163	1599	3 - 164	4286	Asp-13 to Gln-19.	H0059: 2		
HUKEH36	531110	1600	139 - 327	4287		H0059: 2		
HUKEH50	531108	1601	126 - 254	4288	Pro-19 to Pro-28.	H0059: 2, L0657: 1, L0809: 1 and L0789: 1.		
HUKEK55	522213	1602	2 - 271	4289	Ile-49 to Gly-63, Ile-66 to Asp-77, Gly-84 to Ser-90.	H0059: 2 and L0766: 1.		
HUKEO55	714187	1603	253 - 62	4290		H0059: 2		
HUKES11	967604	1604	3 - 122	4291	Arg-1 to Ser-6, Tyr-11 to Asp-17.	H0059: 2		
HUKFL69	526819	1605	103 - 294	4292		H0059: 2		
HUKFV41	537530	1606	3 - 302	4293	Thr-14 to Trp-20, Gly-25 to Pro-30, Gln-42 to Trp-60.	H0059: 2 and L0803: 2.		

HUKFX63	946931	1607	2 - 112	4294	Cys-18 to Ser-24, Gly-29 to Gln-37.	AR061: 69, AR089: 1 H0046: 1 and H0059: 1.		
HUNAD94	575299	1608	1 - 135	4295	Thr-1 to Asn-10, Ser-18 to Lys-31.	T0069: 2		
HUVBB90	503042	1609	184 - 342	4296		H0056: 2		
HUVBB93	502903	1610	145 - 231	4297		H0056: 2		
HUVBC12	933023	1611	122 - 289	4298	Thr-35 to Asn-45.	H0056: 3		
HUVCQ07	928053	1612	3 - 371	4299	Asp-14 to Ala-30, Val-33 to Tyr-39, Ile-52 to Lys-58, Thr-83 to Arg-88.	H0056: 7		
HUVCQ55	868795	1613	163 - 372	4300	Ile-1 to Asn-8.	H0056: 10 and S0134: 1.		
HUVCS14	914768	1614	1 - 243	4301	Asn-1 to Ala-14, Arg-30 to Gly-37.	H0056: 1, H0623: 1 and L0748: 1.		
HUVCU71	968663	1615	79 - 279	4302	Leu-40 to Leu-45, Phe-55 to Leu-60.	H0056: 2		
HUVCW62	535361	1616	139 - 309	4303	Arg-6 to Ala-26.	H0056: 8		
HUVDB28	535006	1617	38 - 220	4304		H0056: 6 and L0547: 1.		
HUVDB53	509119	1618	151 - 297	4305	Gly-1 to Ser-10.	H0056: 2		
HUVDC15	921088	1619	3 - 176	4306		H0056: 11, L0805: 2, L0789: 2, S0358: 1, L0375: 1, L0776: 1, L0743: 1, L0777: 1 and L0759: 1.		
HUVDD09	707061	1620	1 - 177	4307	Pro-27 to Trp-38, Leu-48 to Arg-56.	H0056: 2		

HUVDF13	961020	1621	1 - 225	4308	Arg-1 to Ser-6, Arg-13 to Ser-18.	H0056: 2		
HUVDF84	526248	1622	2 - 214	4309		H0056: 2		
HUVDF88	522823	1623	3 - 257	4310	Gly-1 to Arg-12.	H0056: 3		
HUVDI28	530558	1624	29 - 241	4311	Glu-13 to Phe-18, Gly-46 to Ala-56.	H0056: 2, H0623: 1 and L0439: 1.		
HUVDI76	719332	1625	111 - 293	4312		H0056: 3 and H0623: 3.		
HUVDL30	530387	1626	3 - 110	4313	Lys-16 to Lys-36.	H0056: 2		
HUVDO25	679477	1627	233 - 412	4314	Ser-21 to Thr-29.	H0623: 2, H0056: 1 and L0748: 1.		
HUVDP95	530386	1628	1 - 81	4315	Phe-7 to Trp-22.	H0056: 2 and H0623: 2.		
HUVDS26	958027	1629	224 - 415	4316	Ala-2 to Gly-9.	H0623: 2, H0056: 1 and L0758: 1.		
HUVDU51	868660	1630	3 - 263	4317		H0056: 1 and H0623: 1.		
HUVED35	430750	1631	318 - 572	4318	Lys-31 to Gln-40, Gln-42 to Met-49, Lys-74 to Thr-82.	H0040: 1, H0056: 1, H0623: 1, L0755: 1 and L0592: 1.		
HUVED54	534783	1632	1 - 150	4319		H0056: 2		
HUVED65	527937	1633	75 - 164	4320	Gln-20 to Cys-26.	H0056: 2		
HUVEN50	530094	1634	3 - 110	4321	Arg-12 to Gly-17.	H0056: 2, H0615: 1 and H0623: 1.		
HUVFA55	868779	1635	148 - 354	4322		H0056: 2 and H0623: 1.		
HUVFB48	967815	1636	170 - 343	4323	Leu-22 to Ser-31.	H0056: 1 and H0623: 1.		
HUVFB69	868782	1637	175 - 330	4324		H0056: 1 and H0623:		

HUVFC07	952080	1638	85 - 240	4325	Phe-1 to Gly-8.	1.	H0623: 2 and L0759: 1.		
HUVFH03	922064	1639	240 - 362	4326	Phe-3 to Arg-8, Arg-21 to Ser-27.		H0623: 2		
HUVFH32	934003	1640	160 - 294	4327	Ser-27 to Gly-32.		H0623: 3		
HUVFI03	868776	1641	3 - 131	4328			H0056: 1 and H0623: 1.		
HUVFK11	965765	1642	119 - 328	4329	Ser-46 to Pro-57.		H0623: 2		
HUVFK58	868784	1643	435 - 734	4330	His-7 to Thr-18, Gly-53 to Phe-59, Pro-67 to Ser-74, Val-76 to Leu-85.		H0623: 2, L0749: 2, H0056: 1 and L0794: 1.		
HUVFL71	958059	1644	3 - 128	4331	Asp-1 to Arg-7.		H0623: 2		
HUVFQ03	922727	1645	213 - 374	4332			H0623: 3		
HUVFR02	918233	1646	20 - 286	4333	Thr-3 to Ala-12, Ser-27 to Ala-32, Ala-38 to Glu-44.		H0623: 2 and L0534: 1.		
HUVFT28	870617	1647	97 - 417	4334	Arg-1 to Ser-8, Pro-13 to Pro-18, Glu-55 to Trp-64.		H0623: 3, H0616: 1 and L0748: 1.		
HUVFT50	868769	1648	3 - 371	4335	Asp-1 to Asn-10, Thr-29 to Trp-43, Trp-62 to Ser-68.		H0545: 1 and H0623: 1.		
HUVFZ06	933942	1649	225 - 422	4336	Thr-9 to Asp-17, Asp-43 to Arg-48.		H0623: 2		
HUVGZ77	909169	1650	2 - 382	4337	Lys-1 to Cys-8, Glu-31 to Ser-37, Val-98 to Pro-105.		AR089: 2, AR061: 1, H0623: 2, H0056: 1, L0803: 1, L0750: 1 and		

HUVHB35	868751	1651	145 - 354	4338		L0779: 1. H0056: 1 and H0623: 1.		
HUVHB59	963129	1652	200 - 400	4339	Pro-35 to Ser-46.	H0623: 3		
HUVHC93	908555	1653	51 - 344	4340	Pro-5 to Trp-10, Phe-20 to Met-26, Leu-85 to Trp-92.	AR089: 3, AR061: 1 H0040: 1, H0056: 1 and H0623: 1.		
HUVHD88	868697	1654	158 - 39	4341		H0623: 2		
HUVHG80	968507	1655	33 - 221	4342	Lys-21 to Lys-27.	H0623: 2 and H0056: 1.		
HUVHI07	952090	1656	313 - 522	4343	Leu-23 to Ser-35.	H0056: 1, H0623: 1 and L0367: 1.		
HUVHO40	924621	1657	1 - 486	4344	Leu-51 to Val-56, Ala-69 to Arg-74, Thr-82 to Thr-91, Asp-116 to Ile-126, Ala-142 to Pro-147.	H0623: 2 and L0731: 1.	22q13.33	
HUVHU74	868649	1658	158 - 361	4345	Thr-47 to Arg-53.	H0623: 2		
HVCAZ38	969208	1659	3 - 206	4346	Ala-47 to Phe-55.	H0666: 339, H0660: 3, L0751: 2, H0676: 1, H0560: 1 and H0520: 1.		
HVCBV04	925844	1660	519 - 632	4347	His-1 to Ser-6.	H0666: 5		
HVCCC81	933449	1661	3 - 62	4348		H0666: 2		
HVCCCK04	925796	1662	3 - 560	4349	Arg-8 to Gly-19, Pro-22 to Cys-29, Asp-54 to Cys-65, Ser-68 to Ala-77, Glu-97 to Ser-103, Pro-171 to Leu-176.	H0666: 222, L0776: 5, L0749: 3, S0358: 2, L0763: 2, L0766: 2, L0439: 2, L0596: 2, H0650: 1, H0341: 1, S0442: 1, H0009: 1.		

							H0178: 1, H0012: 1, H0087: 1, S0150: 1, L0805: 1, L0655: 1, L0657: 1, L0659: 1, L0783: 1, L0809: 1, L0789: 1, L0663: 1, S0374: 1, L0602: 1, L0731: 1 and L0758: 1.			
HVVAC41	949141	1663	85 - 273	4350			H0672: 2			
HVVAJ01	914354	1664	83 - 277	4351	Asp-34 to Glu-40.		H0644: 1, H0658: 1 and H0672: 1.			
HVVAJ06	933675	1665	1 - 240	4352			H0672: 2			
HVVBG19	968967	1666	1 - 171	4353			H0672: 2			
HVVBK45	964102	1667	710 - 480	4354	Cys-14 to Tyr-21.		L0666: 3 and H0672: 2.			
HVVBK72	933167	1668	2 - 397	4355	Glu-38 to Lys-43, Gly-125 to Thr-132.		AR061: 1, AR089: 1 H0038: 1, H0672: 1 and L0758: 1.			
HVVBV44	917559	1669	3 - 104	4356			H0672: 2			
HVVCO01	913996	1670	67 - 294	4357	Lys-12 to Trp-18, Phe-35 to Thr-42.		H0672: 2			
HWLHJ68	957834	1671	78 - 410	4358	Cys-17 to Lys-31.		AR089: 3, AR061: 2 H0651: 709, L0766: 5, L0754: 5, L0756: 3, L0803: 2, L0779: 2, L0759: 2, S0354: 1, H0643: 1, H0013: 1, H0194: 1, H0545: 1, H0373: 1, H0252: 1, H0615: 1, H0316: 1,			

							H0040: 1, H0641: 1, H0647: 1, S0422: 1, L0598: 1, L0369: 1, L0520: 1, L0762: 1, L0649: 1, L0804: 1, L0527: 1, L0656: 1, H0144: 1, H0702: 1, H0547: 1, H0555: 1, H0436: 1, S0028: 1, L0746: 1, L0750: 1, L0777: 1, L0780: 1, L0752: 1 and L0686: 1. L0766: 1 and H0672: 1.			
HVVD04	925793	1672	137 - 3	4359			AR089: 14, AR061: 6 H0672: 1			
HVVBY08	957658	1673	2 - 406	4360			L0731: 2, L0635: 1, L0663: 1, H0672: 1 and L0777: 1.			
HVBM06	933528	1674	288 - 443	4361		Pro-33 to Gly-38, Leu-45 to Thr-51.	L0470: 1 and H0623: 1.			
HUVHL82	912011	1675	215 - 580	4362		Glu-28 to Arg-36, Pro-41 to Thr-50.	L0471: 1 and H0623: 1.			
HUVHI06	952479	1676	1856 - 2053	4363			L0766: 3, H0623: 1, L0740: 1, L0745: 1 and L0779: 1.			
HUVGP05	930892	1677	2 - 397	4364		Ala-18 to Arg-25.	H0623: 1 and L0439: 1.			
HUVFP71	950681	1678	443 - 204	4365			AR089: 2, AR061: 2 H0623: 1	6p21.1-p12	179605, 179605,	
HUVFI01	945834	1679	61 - 1212	4366						



								179605, 179605, 179605, 180297, 230450, 248611, 263200, 600364, 601498, 601690
HUVFE03	922889	1680	112 - 258	4367			H0623: 1 and L0777: 1.	
HUVDO18	868783	1681	13 - 177	4368	Gln-26 to Gln-33, Arg-38 to Thr-45.		H0056: 1	
HUVDO11	967813	1682	2 - 277	4369	Ile-1 to Leu-10, Gly-54 to Cys-77.		H0056: 1	
HUVDO07	954224	1683	200 - 313	4370			H0056: 1	
HUVDM27	521938	1684	1 - 144	4371	Gly-12 to Ser-17.		H0056: 1	
HUVDH61	526590	1685	80 - 343	4372	Ser-10 to Arg-15.		H0056: 1	
HUVCU26	974232	1686	420 - 701	4373	Leu-12 to Trp-20, Ile-29 to Val-34, Ser-52 to Arg-60.		H0056: 1	
HUVCM76	522660	1687	1 - 147	4374	Arg-17 to Ser-38.		H0056: 1	
HUVBC21	671479	1688	2 - 199	4375	Lys-1 to Arg-7, Phe-48 to Phe-54.		L0745: 3, L0752: 3, H0056: 1, L0761: 1, L0803: 1, L0749: 1 and L0759: 1.	
HUVAA46	667943	1689	521 - 384	4376			H0055: 1	
HUNAK12	839574	1690	120 - 278	4377			T0069: 1 and L0779: 1.	

HUNAG41	711543	1691	185 - 352	4378	Ser-33 to Ser-38.	L0439: 4 and T0069: 1.	
HUNAF22	800452	1692	3 - 221	4379	Ser-12 to Ile-19, Thr-38 to Pro-46.	AR050: 45, AR051: 39, AR054: 35 T0069: 1	
HUNAF20	961527	1693	171 - 326	4380	Glu-26 to His-35, Pro-44 to Asn-49.	T0069: 1, L0764: 1, L0771: 1, L0783: 1 and L0756: 1.	
HUNAE95	796691	1694	2 - 205	4381		L0754: 4, T0069: 1 and L0599: 1.	
HUNAE76	524239	1695	50 - 214	4382	Ala-8 to Ser-14, Lys-21 to Pro-29.	T0069: 1	
HUNAE02	921132	1696	2 - 388	4383	Thr-26 to Pro-36, Ile-52 to Ser-60.	T0069: 1 and L0764: 1.	
HUNAD10	968590	1697	294 - 491	4384		T0069: 1 and L0766: 1.	
HUNAC68	753817	1698	65 - 199	4385	Asn-1 to Asn-6.	T0069: 1 and L0754: 1.	
HUNAB76	968754	1699	2 - 190	4386		L0748: 2 and T0069: 1.	
HUNAB42	714264	1700	3 - 170	4387	Lys-1 to Asn-9.	T0069: 1 and L0747: 1.	
HUKFS69	754186	1701	53 - 151	4388		H0059: 1 and L0756: 1.	
HUKFL89	574525	1702	1 - 174	4389	Leu-32 to Tyr-38.	H0059: 1 and L0752: 1.	
HUKFL71	760581	1703	2 - 241	4390	Gly-19 to Ser-24.	H0059: 1	
HUKFL52	574523	1704	67 - 213	4391		H0059: 1	
HUKFK53	577349	1705	263 - 433	4392		AR054: 9, AR050: 2, AR051: 1 H0059: 1	
HUKFE56	574381	1706	83 - 226	4393		H0059: 1 and L0747: 1.	
HUKFD95	796014	1707	47 - 364	4394	Arg-26 to Arg-31.	L0766: 2 and H0059:	

HUKEY01	921504	1708	29 - 178	4395	Pro-7 to Gly-18.	1. H0059: 1 and L0779:		
HUKER62	772501	1709	532 - 119	4396		1. H0059: 1 and L0439:		
HUKEP18	957456	1710	852 - 265	4397		1. AR061: 14, AR054: 11, AR050: 9, AR089: 4 L0758: 2, H0059: 1, L0789: 1, L0665: 1, L0749: 1 and L0779: 1.		
HUKDY02	920815	1711	234 - 482	4398		H0059: 1, L0439: 1 and L0747: 1.		
HUKDU47	719465	1712	33 - 185	4399	Met-23 to Gly-34, Glu-40 to Ser-50.	L0455: 1, H0059: 1 and L0753: 1.		
HUKDG10	968333	1713	3 - 329	4400		L0465: 2 and H0059: 1.		
HUKCP30	690933	1714	1 - 105	4401	Lys-27 to His-35.	H0059: 1, L0657: 1 and L0748: 1.		
HUKCO11	967742	1715	76 - 450	4402	Arg-1 to Asp-7, Glu-26 to Ser-31, Glu-51 to Val-56, Asp-59 to Val-69, Glu-85 to Asn-94.	L0766: 2, H0059: 1, L0764: 1 and L0774: 1.		
HUKCL85	529718	1716	77 - 229	4403	Phe-8 to Glu-15, Val-20 to Thr-25, Cys-40 to Glu-49.	H0059: 1		
HUKCC25	529723	1717	84 - 260	4404		H0059: 1		
HUKCC15	518537	1718	2 - 106	4405	Pro-18 to Cys-25.	H0059: 1		

HUKAT59	628540	1719	399 - 136	4406	Arg-16 to Cys-22, Pro-83 to Thr-88.	H0059: 1		
HUKAQ76	502711	1720	351 - 178	4407		H0059: 1 and L0748: 1.		
HUKAO47	502911	1721	379 - 170	4408		L0748: 2 and H0059: 1.		
HUKAM19	672076	1722	150 - 329	4409	Ala-47 to Thr-53.	H0059: 1		
HUKAM18	502912	1723	314 - 117	4410	Asp-34 to Arg-41, Glu-44 to Lys-50.	H0059: 1, L0800: 1, L0794: 1, L0789: 1, L0747: 1, L0750: 1 and L0362: 1.		
HUKAL44	716927	1724	139 - 402	4411	Arg-1 to Gln-7, Gln-11 to Ser-17, Ser-41 to His-46.	H0059: 1, L0775: 1, L0664: 1 and L0592: 1.		
HUKAJ91	790487	1725	159 - 1	4412		L0750: 2 and H0059: 1.		
HUKAJ83	524257	1726	317 - 102	4413	Lys-1 to Gln-8.	H0059: 1		
HUKAD77	772734	1727	2 - 421	4414	Ser-30 to Val-38, Gln-44 to Ser-53, Pro-56 to Gly-63.	H0059: 1 and L0755: 1.		
HUKAB63	625273	1728	1 - 207	4415	Trp-10 to Gly-16.	H0059: 1		
HUKAB25	677470	1729	274 - 2	4416		H0059: 1, L0520: 1, L0753: 1 and L0731: 1.		
HUKAA54	503630	1730	369 - 67	4417		H0059: 1		
HUKAA39	503627	1731	286 - 2	4418		L0439: 2 and H0059: 1.		
	503628	2659	156 - 434	5346				
HUDBZ01	869026	1732	213 - 533	4419	Arg-7 to Arg-13, Asn-31 to Ser-37.	AR050: 75, AR054: 59, AR051: 51		

	915945	2660	191 - 3	5347			S0042: 1		
HUDBK39	886368	1733	77 - 487	4420	Gly-43 to Leu-48, Ser-57 to Lys-67.		AR054: 2, AR051: 0, AR050: 0 S0042: 1 S0042: 1 S0042: 1 S0042: 1		
HUDBE95	795796	1734	147 - 248	4421					
HUDBE64	746508	1735	56 - 286	4422					
HUDBE48	869034	1736	39 - 368	4423	Glu-17 to Ala-30, Gly-42 to Thr-56.		S0042: 1		
HUDBE28	686520	1737	3 - 374	4424	Glu-1 to Leu-6, Cys-10 to Asn-28, Lys-41 to Tyr-50, Gln-53 to Ser-60, Pro-67 to His-78.		S0042: 1		
HUDBE02	917361	1738	3 - 137	4425	Phe-2 to Arg-7, Asn-23 to Asn-32, Gln-39 to Asn-45.		S0042: 1		
HUDAK54	899753	1739	18 - 710	4426	Thr-14 to Phe-26, Gln-46 to Arg-52, Leu-74 to Tyr-84, Glu-125 to Glu-132, Tyr-180 to Ser-186, Leu-216 to Pro-222, Val-226 to His-231.		AR051: 32, AR050: 31, AR054: 25 S0042: 1		
HUDAK19	671974	1740	109 - 234	4427	Glu-27 to Glu-33.		L0783: 1, L0439: 1, L0731: 1 and S0042: 1.		
HTTKG12	969547	1741	1 - 171	4428	Thr-1 to Ser-10.		H0634: 1 and L0593: 1.		
HTTKC85	956206	1742	380 - 240	4429			H0634: 1, L0662: 1 and L0766: 1.		

HTTJV79	869602	1743	61 - 213	4430		H0634: 1 and L0766: 1.		
HTTJN26	869612	1744	132 - 497	4431	Glu-53 to Gln-62, Gly-80 to Val-86.	L0770: 3, L0777: 3, L0518: 2, L0779: 2, L0758: 2, L0608: 2, H0634: 1, L0764: 1, L0803: 1, L0749: 1 and L0752: 1.		
HTTJK06	934094	1745	2 - 577	4432	Gln-1 to Trp-16, Asp-18 to Gly-25, Leu-38 to Pro-43, Trp-146 to Gly-153.	H0634: 1 and L0565: 1.		
HTTIX05	931024	1746	395 - 532	4433		H0634: 1, L0803: 1, L0749: 1 and L0779: 1.		
HTTIR33	974323	1747	136 - 345	4434	Lys-11 to Glu-18.	H0634: 1		
HTTIR04	926772	1748	86 - 235	4435		H0634: 1, L0766: 1 and L0588: 1.		
HTTIN11	965920	1749	452 - 625	4436		L0745: 2 and H0634: 1.		
HTTIE08	958169	1750	195 - 329	4437	Ala-10 to Thr-16.	H0634: 1 and L0731: 1.		
HTTIB12	969568	1751	1 - 216	4438	Pro-25 to Thr-31, Pro-59 to Gly-72.	H0634: 1 and L0748: 1.		
HTTHJ56	944914	1752	87 - 218	4439	Asn-1 to Arg-11, Val-23 to Ser-28, Asp-35 to Tyr-44.	L0157: 1 and H0634: 1.		
HTTIFG12	751809	1753	128 - 373	4440	Leu-21 to Gly-30.	H0040: 1		
HTTEZ61	742004	1754	146 - 301	4441	Ser-24 to His-34.	H0040: 1 and L0439: 1.		

HTTEQ59	739445	1755	57 - 230	4442			H0040: 1, L0766: 1 and L0748: 1.		
HTTEQ01	917156	1756	2 - 205	4443	Pro-28 to Thr-38, Gly-47 to Arg-52.		H0040: 1, L0803: 1, L0439: 1 and L0777: 1.		
HTTEO59	900662	1757	1 - 153	4444	Gly-1 to Asp-8, Leu-15 to Cys-20, Gly-24 to Ser-29.		AR061: 5, AR089: 5 H0040: 1		
HTTEO53	728344	1758	396 - 545	4445	Arg-2 to Ile-8, Ser-34 to Cys-44.		H0040: 1, L0740: 1 and L0747: 1.		
HTTEJ56	573669	1759	1 - 339	4446	Pro-1 to Glu-7, Thr-29 to Gly-35, Glu-63 to Ile-68, Glu-89 to Asn-95, Glu-98 to Leu-105.		AR050: 2, AR051: 1, AR054: 0 L0439: 3 and H0040: 1.		
HTTEB05	932294	1760	1 - 387	4447	Arg-10 to Asp-15.		L0483: 1 and H0040: 1.		
HTTDO59	744438	1761	511 - 747	4448	Arg-1 to Trp-9, Pro-13 to Gly-19, Gly-24 to Pro-32.		L0754: 2 and H0040: 1.	1q21	104770, 107670, 110700, 135940, 145001, 146790, 152445, 152445, 159001, 174000, 179755, 182860, 182860, 182860,

								191315, 230800, 230800, 266200, 600897, 601105, 601412, 601652, 602491
HTTDM42	460948	1762	177 - 401	4449				AR061: 5, AR089: 5 L0748: 2 and H0040: 1.
HTTDL81	694222	1763	2 - 241	4450	Ala-4 to Pro-22.			H0040: 1 and L0748: 1.
HTTDL75	766551	1764	41 - 178	4451	Gly-10 to Cys-16, Arg-25 to Trp-31, Pro-39 to Pro-46.			H0040: 1, L0742: 1 and L0592: 1.
HTTDA85	784537	1765	3 - 392	4452	Arg-83 to Arg-88.			H0040: 1 and L0748: 1.
HTTCQ95	796674	1766	2 - 241	4453	Cys-19 to Pro-29.			H0040: 1 and L0755: 1.
HTTCJ39	709581	1767	63 - 266	4454	Ala-50 to Asp-55.			L0745: 2 and H0040: 1.
HTTCD06	960599	1768	162 - 413	4455	Lys-15 to Asn-23, Asp-75 to Val-82.			L0754: 2 and H0040: 1.
HTTCB87	524841	1769	3 - 236	4456	Pro-7 to Ala-26.			H0040: 1 and L0748: 1.
HTTBR42	714220	1770	3 - 272	4457				H0040: 1 and L0592: 1.
HTTBP62	932997	1771	1 - 615	4458	Arg-12 to Gly-20,			L0764: 2 and H0040: 1.



						His-102 to Ser-108, Ala-132 to Gln-137.	1.			
HTTBO82	780164	1772	367 - 170	4459		Asn-24 to Asp-32.	H0040: 1 and L0748: 1.			
HTTBM03	925409	1773	11 - 202	4460		Arg-18 to Trp-29.	H0040: 1 and L0753: 1.			
HTTBI80	781590	1774	3 - 203	4461		Asp-1 to Gln-14, Phe-18 to Gly-33.	H0040: 1 and L0766: 1.			
HTTBH95	530559	1775	125 - 256	4462		Tyr-1 to Tyr-12.	H0040: 1			
HTTBH75	767520	1776	175 - 435	4463			H0040: 1 and L0439: 1.			
HTTBH36	530567	1777	186 - 311	4464			H0040: 1			
HTTAQ60	742377	1778	367 - 627	4465		Asn-1 to Cys-12, Asp-20 to Trp-37.	L0748: 3 and H0040: 1.			
HTTAP45	717736	1779	65 - 262	4466			H0040: 1			
	869717	2661	151 - 342	5348						
HTTAP21	671488	1780	632 - 787	4467			L0747: 2 and H0040: 1.			
HTTAP09	826343	1781	252 - 440	4468			H0040: 1 and L0591: 1.			
HTTAN34	509454	1782	111 - 230	4469		Ser-4 to Lys-12.	L0595: 2, H0040: 1 and L0794: 1.			
HTTAJ93	791413	1783	220 - 420	4470			L0748: 2 and H0040: 1.			
HTTAH03	965134	1784	73 - 294	4471		Ile-15 to Phe-21, Pro-31 to Cys-39, Pro-41 to Pro-49, Leu-69 to Pro-74.	L0769: 2 and H0040: 1.			
HTTAC77	772735	1785	435 - 632	4472			L0752: 2, H0040: 1			

HTTAA94	793001	1786	2 - 271	4473	Asn-14 to Leu-20, Gln-30 to Pro-46.	and L0756: 1. L0749: 2, H0040: 1, L0748: 1 and L0591: 1.		
HTTAA39	710355	1787	298 - 137	4474		H0040: 1 and L0731: 1.		
HTLIP06	934207	1788	20 - 241	4475		H0618: 1, L0751: 1 and L0758: 1.		
HTLID06	974047	1789	318 - 491	4476	Gln-10 to Ser-16.	H0618: 1		
HTLHV59	965808	1790	41 - 277	4477	Pro-8 to Ala-15, Arg-23 to Glu-35, Pro-41 to Val-49.	H0618: 1 and L0731: 1.		
HTLHU81	870150	1791	1 - 345	4478		L0591: 2 and H0618: 1.		
HTLHU63	870147	1792	219 - 527	4479	Glu-33 to Arg-40.	L0439: 3 and H0618: 1.		
HTLHS69	870152	1793	144 - 593	4480	Lys-34 to Pro-40, Glu-51 to Gly-56, Glu-117 to Gly-124.	H0618: 1 and L0770: 1.		
HTLHS05	933720	1794	724 - 113	4481	Pro-42 to Ser-47, Ala-51 to Arg-68, Leu-109 to Gly-117.	H0618: 1 and L0771: 1.		
HTLHK57	894863	1795	736 - 1140	4482	Phe-10 to Pro-19, Gly-107 to Arg-112, Thr-128 to Lys-135.	AR054: 35, AR051: 24, AR050: 10, AR061: 8, AR089: 3 H0618: 1, L0766: 1 and L0749: 1.		
	946914	2662	1342 - 1788	5349	Ser-49 to Lys-58, Glu-75 to Pro-91.			
HTLHJ51	865399	1796	165 - 878	4483	Gln-3 to Arg-10,	H0618: 1, L0749: 1		

						Leu-74 to Arg-80, Pro-87 to Cys-92, Ser-144 to Pro-158.			and L0759: 1.		
HTLHB93	945862	1797	1 - 375	4484		Glu-1 to Glu-6.			AR061: 1, AR089: 1 H0618: 1 and L0758: 1.		
HTLHA63	870172	1798	243 - 566	4485					H0618: 1 and L0779: 1.		
HTLGS10	963458	1799	1 - 483	4486		Ser-25 to Asn-32, His-40 to Glu-45.			L0769: 2 and H0618: 1.		
HTLGR32	928245	1800	657 - 950	4487		Arg-14 to Gly-29.			L0779: 3, L0758: 3, H0618: 1 and L0600: 1.		
HTLGP84	782194	1801	1 - 393	4488		Ser-1 to Lys-12, Met-22 to Gly-29, Pro-62 to Gly-69.			L0439: 3, L0753: 3, H0618: 1, L0741: 1, L0745: 1 and L0746: 1.		
HTLGK08	958304	1802	182 - 388	4489		Glu-35 to Ile-51.			H0618: 1 and L0758: 1.		
HTLGC43	870228	1803	3 - 350	4490		Glu-1 to His-15, Gly-21 to Cys-26, Thr-34 to Pro-42, Pro-49 to Glu-57.			L0794: 2, H0618: 1 and L0768: 1.		
HTLEQ92	932882	1804	3 - 305	4491					L0439: 3 and H0253: 1.		
HTLEP21	671151	1805	3 - 416	4492		Val-25 to Ala-31.			H0253: 1 and L0767: 1.		
HTLEN77	772363	1806	90 - 422	4493		Ala-1 to Ala-35.			AR089: 33, AR061: 18 L0748: 2 and H0253: 1.		
HTLEM92	573400	1807	1 - 429	4494		Gly-1 to Arg-13, Phe-19 to Arg-33.			H0253: 1		

	792812	2663	360 - 599	5350	Glu-28 to Val-34, Trp-58 to Ser-64.			
HTLEL16	384492	1808	2 - 355	4495	Thr-30 to Glu-35, Asp-101 to Gly-106, Ser-112 to Ser-117.	H0253: 1 and L0439: 1.		
HTLEG67	751842	1809	138 - 317	4496	Thr-6 to Ser-11.	L0748: 2 and H0253: 1.		
HTLDZ81	778180	1810	3 - 296 -	4497	Ser-5 to Arg-17.	H0253: 1		
HTLDW27	961353	1811	197 - 601	4498	His-1 to Cys-8, His-35 to Phe-40.	H0253: 1, L0761: 1, L0649: 1 and L0805: 1.		
HTLDO01	913669	1812	3 - 308	4499	Glu-63 to Ala-68, Gly-84 to Tyr-102.	L0758: 3 and H0253: 1.		
HTLDG43	715439	1813	1 - 132	4500	Ala-28 to Trp-33.	H0253: 1		
HTLDB18	868533	1814	2 - 448	4501	Ser-13 to Gly-19, Leu-22 to Asn-36, Asn-57 to Ser-68, Pro-82 to Trp-107.	H0253: 1 and L0439: 1.		
HTLCZ79	572853	1815	1 - 285	4502	Asp-72 to Leu-78.	H0253: 1		
HTLCX66	578921	1816	23 - 199	4503	Gly-6 to Thr-12, Pro-28 to Arg-34, Asn-39 to Asn-47.	H0253: 1		
HTLCO02	921045	1817	152 - 382	4504	Arg-50 to Trp-58.	H0253: 1 and L0768: 1.		
HTLCG65	413333	1818	3 - 143	4505	Ala-14 to Asn-22.	H0253: 1		
HTLCG59	530039	1819	6 - 218	4506		H0253: 1		
HTLCA03	870290	1820	50 - 250	4507		H0253: 1		
HTLBH67	751985	1821	1 - 282	4508		AR061: 2, AR089: 1 L0752: 3, L0747: 2, H0294: 1, H0253: 1,		

							H0046: 1, H0040: 1, H0063: 1, H0494: 1, S0352: 1, L0769: 1, L0766: 1, L0804: 1, L0805: 1, L0791: 1, H0521: 1, L0779: 1, L0780: 1, L0731: 1 and L0758: 1.			
HTLBC07	954111	1822	259 - 408	4509			L0758: 2 and H0253: 1.			
HTLBB72	766270	1823	3 - 590	4510		His-1 to Trp-11, Lys-13 to Ser-27, Glu-33 to Ser-38.	H0253: 1, L0745: 1 and L0750: 1.			
HTLAI30	690936	1824	133 - 492	4511			L0439: 3, L0438: 2, H0253: 1 and L0769: 1.			
HTLAF33	870300	1825	1 - 228	4512		Phe-2 to Arg-12.	H0253: 1			
HTLAC61	683247	1826	28 - 165	4513			H0253: 1	6p25-pter		
HTLAC39	575343	1827	74 - 226	4514		Ala-1 to Trp-18.	H0253: 1			
HTLAB55	732480	1828	3 - 320	4515		Gln-32 to Leu-37, Gln-65 to Val-70, Thr-73 to Pro-79.	H0253: 1 and L0439: 1.			
HTLAB29	879168	1829	133 - 426	4516		Gly-1 to Thr-9.	H0253: 1 and L0747: 1.			
HTFBE02	920507	1830	1 - 363	4517		Asp-28 to Leu-35, Asp-52 to Cys-57.	AR089: 1, AR061: 0 L0439: 2, L0021: 1, H0372: 1, L0769: 1, L0649: 1, L0748: 1, L0485: 1, L0604: 1 and L0361: 1.			
HTEQS95	972746	1831	311 - 496	4518		Ser-37 to Ser-43.	H0616: 1			

HTEQS90	973426	1832	86 - 388	4519	Pro-45 to Pro-50, Arg-64 to Ser-77, Ile-88 to Ala-101.	H0616: 1		
HTEQP03	870516	1833	129 - 596	4520	Pro-71 to Cys-82.	H0616: 1 and L0794: 1.		
HTEQN83	908528	1834	3 - 293	4521	Met-12 to Met-24, Pro-46 to Tyr-52, Arg-92 to Lys-97.	AR061: 4, AR089: 1 L0758: 2 and H0616: 1.		
HTEQB08	958291	1835	147 - 437	4522	Val-48 to Gly-54, Asp-63 to Arg-74, Gly-87 to Leu-92.	L0748: 2, H0616: 1 and L0747: 1.		
HTEPY28	870559	1836	263 - 412	4523	Ala-1 to Met-6, Gly-9 to Ser-15.	L0758: 3 and H0616: 1.		
HTEPV63	870549	1837	614 - 931	4524	Leu-47 to Thr-59, Pro-73 to Pro-87.	H0616: 1, L0519: 1, L0748: 1 and L0779: 1.		
HTEPE35	948475	1838	839 - 78	4525	Tyr-1 to Lys-8, Phe-19 to Ser-24, Thr-28 to Ser-34, Pro-54 to Trp-70.	AR061: 4, AR089: 1 L0758: 7, L0768: 2, H0616: 1 and L0151: 1.		
HTEOY82	948845	1839	159 - 392	4526		H0616: 1 and L0779: 1.		
HTEOO83	836721	1840	1 - 318	4527	Lys-22 to Asp-27.	H0616: 1 and L0774: 1.		
HTEOE28	870581	1841	18 - 296	4528	Leu-80 to Lys-86.	H0616: 1 and L0779: 1.		
HTENY44	870588	1842	3 - 191	4529	Asp-16 to Arg-23, Leu-40 to Asp-47.	L0758: 3, H0616: 1, L0794: 1, L0791: 1 and L0779: 1.		
HTENV06	933294	1843	133 - 390	4530	Glu-1 to Ser-10.	H0616: 1 and L0755: 1.		

HTENS74	773925	1844	3 - 329	4531	Arg-30 to Arg-37, Asn-40 to Glu-46, Leu-56 to Arg-64, Ala-85 to Arg-102.	L0755: 2 and H0616: 1.	17p13.3	113721, 247200, 600059, 601545
HTENR26	870595	1845	15 - 146	4532	Thr-12 to Ile-17.	H0616: 1 and L0768: 1.		
HTENQ92	790908	1846	54 - 494	4533	Ala-6 to Trp-19, Leu-34 to Gln-39, Asp-63 to Arg-76, Thr-94 to Gly-105, Asp-108 to Phe-113, Lys-122 to Phe-128, Asn-131 to Glu-136, Arg-142 to Gly-147.	L0731: 3, H0616: 1 and L0750: 1.		
HTENP08	958382	1847	58 - 447	4534	Tyr-2 to His-7.	H0616: 1 and L0794: 1.		
HTENL95	795314	1848	149 - 322	4535	Pro-43 to Ile-51.	L0748: 2, H0616: 1, L0439: 1 and L0740: 1.		
HTENL73	974363	1849	109 - 426	4536	Pro-29 to Thr-34, Cys-42 to Ser-47, Gln-52 to His-58, Pro-68 to Cys-80.	H0616: 1		
HTENA08	958380	1850	60 - 206	4537		H0616: 1 and L0758: 1.		
HTEMY05	880592	1851	1 - 363	4538	Cys-18 to Lys-43, Ser-45 to Leu-52, Ser-63 to Ser-68, Lys-75 to Arg-80, His-113 to Lys-121.	H0616: 1 and L0362: 1.		
HTEMV66	813038	1852	1 - 318	4539	Ser-38 to Pro-45.	AR061: 5, AR089: 1		

HTEMU66	944419	1853	454 - 963	4540	Ala-1 to Gln-7, Lys-24 to Ser-30, Pro-44 to Asn-53, Glu-104 to Asp-112, Leu-152 to Ser-157.	H0616: 1 and L0758: 1. AR061: 7, AR089: 5 H0616: 1		
HTEMS01	915308	1854	21 - 197	4541	Glu-3 to Cys-9, Gln-32 to Asp-45.	L0758: 4 and H0616: 1.		
HTEMO58	964769	1855	77 - 361	4542		H0616: 1 and L0758: 1.		
HTEMN80	775543	1856	51 - 137	4543		H0616: 1 and L0439: 1.		
HTEMM91	938396	1857	58 - 378	4544	His-15 to Arg-22.	H0616: 1 and L0747: 1.		
HTEMI51	870613	1858	283 - 573	4545	Arg-24 to Pro-30.	H0616: 1, L0779: 1 and L0758: 1.		
HTEMB57	849214	1859	198 - 374	4546	His-44 to Phe-49, Pro-53 to Pro-58.	H0616: 1 and L0758: 1.		
HTELY90	787549	1860	2 - 250	4547		H0616: 1 and L0748: 1.		
HTELV29	806421	1861	33 - 641	4548	Pro-28 to His-34, Lys-51 to Arg-59, Arg-66 to Phe-82, Thr-92 to Gln-100, Ala-106 to Gln-118, Pro-123 to Leu-133, Ala-137 to Glu-147, Arg-185 to Leu-190.	H0616: 1 and L0594: 1.		
HTELP07	952274	1862	102 - 296	4549	Thr-15 to Lys-28,	H0616: 1, L0764: 1,		



HTELM71	954982	1863	63 - 329	4550	Gly-47 to Thr-54. Pro-24 to Asn-37, Asp-43 to Thr-49, Leu-63 to Gln-72.	L0779: 1 and L0758: 1. L0758: 2 and H0616: 1.		
HTELA02	918699	1864	185 - 451	4551	Ala-48 to Lys-57, Ser-75 to Phe-84.	L0794: 2, H0616: 1 and L0758: 1.		
HTEKU62	754010	1865	43 - 657	4552	His-1 to Lys-7.	H0038: 1 and L0439: 1.		
HTEKI62	812862	1866	68 - 286	4553	Pro-43 to Asn-48.	L0766: 2, H0038: 1, L0637: 1, L0750: 1 and L0590: 1.		
HTEKH17	942526	1867	83 - 391	4554		AR051: 29, AR050: 21, AR054: 21, AR089: 11, AR061: 11 H0038: 1		
HTEKD77	772397	1868	105 - 428	4555	Ala-5 to Arg-15.	H0038: 1 and L0756: 1.		
HTEJV94	793039	1869	92 - 241	4556	Pro-19 to Phe-28.	L0758: 2 and H0038: 1.		
HTEJO46	717850	1870	282 - 401	4557	Ser-5 to Cys-16, Glu-20 to Ile-25.	H0038: 1 and L0743: 1.		
HTEJN12	653252	1871	1 - 279	4558		H0038: 1 and L0595: 1. Xp22	300000, 300066, 300077, 300310, 301220, 302350, 304050, 304110, 306100,	

HTEJL30	696784	1872	23 - 301	4559				L0748: 2 and H0038: 1.	15q21.1-q21.2	309530, 309585, 312040
										107910, 107910, 109700, 114240, 134797, 134797, 134797, 151670, 600839, 601780, 602099
HTEJC70	490772	1873	601 - 380	4560				H0038: 1 and L0748: 1.		
	870649	2664	1 - 330	5351			Arg-1 to Arg-6, Pro-17 to Ala-23, Gly-33 to Gln-40, Arg-45 to Arg-73.			
HTEJB07	953801	1874	79 - 264	4561			Thr-1 to Glu-7, Cys-35 to Gly-51.	L0779: 3, L0758: 2 and H0038: 1.		
HTEIS34	887112	1875	383 - 135	4562			Cys-33 to Asn-38.	H0038: 1 and L0366: 1.		
HTEIS25	870660	1876	3 - 299	4563			Pro-31 to Arg-37, Phe-39 to Ala-55.	L0758: 4 and H0038: 1.		
HTEIN26	684711	1877	178 - 417	4564			Gly-1 to Glu-9, Ile-12 to Lys-30, Cys-34 to Lys-39, Glu-55 to Gln-62,	H0038: 1 and L0754: 1.		

HTEIL36	708304	1878	69 - 395	4565	Val-66 to Lys-72.	H0038: 1, L0768: 1, L0438: 1 and L0779: 1.		
HTEIJ58	491030	1879	379 - 179	4566	Asp-19 to Ser-25.	H0038: 1		
	870667	2665	3 - 281	5352	Ile-1 to Phe-9, Gly-73 to Gly-82.			
HTEID15	395868	1880	44 - 151	4567	Gln-1 to Leu-6.	H0038: 1		
HTEIB38	839966	1881	39 - 296	4568	His-1 to Asp-9, Lys-37 to Glu-45.	H0038: 1 and L0779: 1.		
HTEIB37	870671	1882	19 - 264	4569	Gln-11 to Cys-18.	H0038: 1		
HTEIB03	921926	1883	35 - 235	4570	Pro-2 to Thr-13.	H0038: 1		
HTEIA57	734983	1884	1 - 225	4571	Glu-1 to Ser-18.	L0748: 2 and H0038: 1.		
HTEHX57	734976	1885	279 - 446	4572	Gly-14 to Val-21, Thr-25 to Leu-32.	H0038: 1, L0740: 1 and L0754: 1.		
HTEHV11	967439	1886	59 - 361	4573	Gln-9 to Ala-21, Thr-24 to Thr-29.	H0038: 1, L0779: 1 and L0758: 1.		
HTEHS17	664436	1887	15 - 233	4574	Lys-30 to Leu-39, Glu-42 to Ser-53.	L0758: 3, L0151: 2, H0038: 1 and L0779: 1.		
HTEHJ11	964956	1888	147 - 254	4575	Gly-10 to Arg-19.	L0163: 1 and H0038: 1.		
HTEGW02	920628	1889	64 - 747	4576	Lys-1 to Arg-27, Thr-42 to Met-57, Gln-89 to Ala-95, Asp-113 to Ser-119, Thr-128 to Thr-156, Phe-179 to Ser-187.	L0758: 3, L0776: 2, L0779: 2 and H0038: 1.		
HTEGU55	931017	1890	173 - 388	4577	Ala-1 to Lys-10, Pro-29 to Ser-36,	L0439: 2 and H0038: 1.	20q13.12	602025

							Gly-46 to Ser-58, Ile-62 to Cys-67.					
HTEGS24	932987	1891	130 - 600	4578			Glu-13 to Ser-20, Pro-33 to Phe-38, Ser-41 to Lys-49.				H0038: 1 and L0766: 1.	
HTEGJ74	765901	1892	3 - 452	4579							AR089: 3, AR061: 2 L0439: 2 and H0038: 1.	
HTEGJ56	732630	1893	272 - 457	4580			Asp-26 to Trp-35.				H0038: 1 and L0755: 1.	
HTEGJ38	709420	1894	74 - 325	4581							H0038: 1 and L0749: 1.	
HTEGH60	545137	1895	3 - 221	4582			Gly-5 to Gly-12.				H0038: 1	
HTEGC30	690998	1896	2 - 97	4583							H0038: 1 and L0756: 1.	
HTEFX90	887616	1897	3 - 581	4584							AR050: 9, AR051: 3, AR054: 1 H0038: 1, L0750: 1 and L0755: 1.	
HTEFU18	666920	1898	3 - 353	4585			Leu-25 to Asp-35, Ser-41 to Tyr-47, Trp-72 to Pro-77, Lys-106 to Arg-112.				H0038: 1, L0766: 1, L0789: 1 and L0749: 1.	
HTEFO46	719280	1899	133 - 408	4586			Pro-28 to Tyr-38, Thr-40 to Lys-48, Val-61 to Thr-68, Glu-74 to Gln-82.				L0591: 2, H0038: 1, L0381: 1, L0779: 1 and L0758: 1.	
HTEFO28	685383	1900	150 - 464	4587			Thr-6 to Gln-12.				H0038: 1, L0744: 1 and L0756: 1.	
HTEEU78	530196	1901	2 - 256	4588			Ile-1 to Ala-7.				H0038: 1	

HTEEU35	707717	1902				Arg-26 to Gly-38.				
HTEEU27	575476	1903	2 - 115	4589		Glu-15 to Ser-20.		H0038: 1		
HTEEU18	530203	1904	99 - 227	4590		Ser-14 to Ser-25, Leu-42 to Glu-62, Ala-75 to Thr-84.		H0038: 1		
			2 - 280	4591				H0038: 1 and L0758: 1.	1p21	102770, 120280, 120280, 166600, 170995, 232400, 232400, 600309, 601414, 601691, 601691, 601691, 601691, 601718, 602094
HTEEU17	530200	1905	76 - 303	4592		Pro-40 to Leu-50, Ser-64 to Gln-74.		H0038: 1		
HTEET22	675071	1906	206 - 373	4593		Thr-20 to His-29, Pro-31 to Ser-38.		H0038: 1, L0756: 1 and L0758: 1.		
HTEEF25	677513	1907	123 - 341	4594				H0038: 1, L0794: 1 and L0758: 1.		
HTEEB82	780161	1908	151 - 288	4595		Ser-11 to Arg-19.		L0748: 2 and H0038: 1.		
HTEDX39	530201	1909	123 - 260	4596				H0038: 1		
HTEDX04	927850	1910	114 - 344	4597				H0038: 1		
HTEDX03	925353	1911	1 - 204	4598				H0038: 1		
HTEDW96	881958	1912	86 - 511	4599		Thr-48 to Ser-53,		L0601: 2 and H0038: 2q37.2		

						Gly-63 to Arg-68, Gly-77 to Trp-85, Gln-99 to Gly-112, Arg-131 to Arg-142.	1.		
HTEDW59	530448	1913	1 - 213	4600		Gly-17 to Glu-29.	H0038: 1		
HTEDV86	785818	1914	86 - 322	4601		Ser-47 to Phe-57.	H0038: 1 and L0749:		
HTEDU53	727362	1915	2 - 253	4602		Gly-22 to Arg-28.	1. H0038: 1 and L0756: 1.		
HTEDS40	934047	1916	147 - 509	4603			H0038: 1		
HTEDS06	960645	1917	625 - 170	4604			H0038: 1 and L0779:		
HTEDO75	767024	1918	60 - 197	4605			1. H0038: 1		
HTEDK72	766343	1919	137 - 283	4606			H0038: 1 and L0740:		
HTEDI92	522827	1920	3 - 143	4607			1. H0038: 1		
HTEDI63	508086	1921	29 - 322	4608			H0038: 1		
HTEDI09	522969	1922	233 - 409	4609			H0038: 1		
HTEDI01	961028	1923	92 - 229	4610			H0038: 1		
HTEDH90	909165	1924	3 - 311	4611		Phe-1 to Pro-7, Trp-32 to Thr-39.	AR061: 3, AR089: 1 H0038: 1		
HTEDH76	522940	1925	3 - 170	4612		Gly-2 to Ile-13.	H0038: 1		
HTEDH42	615250	1926	18 - 353	4613		Leu-56 to Leu-63, Gly-103 to Arg-108.	AR061: 6, AR089: 4 H0038: 1		
HTEDH30	522936	1927	1 - 249	4614		Asn-1 to Gly-17.	H0038: 1		
HTEDH17	522938	1928	80 - 385	4615		Pro-67 to Gly-75.	H0038: 1		
HTEDH06	869427	1929	2 - 361	4616		Ile-1 to Lys-9, Pro-88 to Lys-100.	H0038: 1		
HTEDG75	890715	1930	162 - 371	4617		Arg-43 to Thr-50.	AR050: 42, AR054:		

HTEDG26	519947	1931	1 - 396	4618	Asn-1 to Arg-8, Leu-18 to Asp-23, Glu-84 to His-89.	35, AR051: 33 H0038: 1 H0038: 1		
HTEDF96	614726	1932	1 - 174	4619	Leu-22 to Arg-34.	H0038: 1	19q13.3	113900, 126340, 126391, 130410, 134790, 138570, 160900, 173850, 258501, 600040, 602225, 602225
HTEDF70	522977	1933	2 - 277	4620	Ile-1 to Gln-11.	H0038: 1		
HTEDF60	742368	1934	1 - 369	4621	Glu-1 to Gln-7, Arg-16 to Asp-30, Pro-35 to Asn-43.	H0038: 1		
HTEDF22	908406	1935	1 - 303	4622	Pro-2 to Trp-7, His-28 to Gly-35, Pro-37 to Gly-56, Gly-68 to Lys-75.	AR061: 8, AR089: 3 L0758: 2 and H0038: 1.		
HTECE66	522997	1936	26 - 196	4623	Gly-36 to Gly-52.	H0038: 1		
HTECE62	523002	1937	1 - 369	4624	Ala-22 to Gly-30, Asn-36 to Ala-43.	H0038: 1		
HTECE61	789732	1938	85 - 471	4625	Ser-30 to Arg-36.	H0038: 1 and L0750: 1.		

HTECE51	870723	1939	85 - 282	4626	Leu-30 to Arg-40.	H0038: 1		
HTECE39	650885	1940	63 - 401	4627	Ser-37 to Gly-49.	H0038: 1		
HTECE31	508104	1941	33 - 203	4628		H0038: 1		
HTECE08	960428	1942	2 - 154	4629	Ile-1 to Ser-8, Pro-13 to Ser-19, Gly-31 to Ile-41.	H0038: 1		
HTECD94	527210	1943	1 - 330	4630	Val-28 to Cys-55, Arg-71 to Cys-90, Pro-102 to Pro-107.	H0038: 1	7q11-q22	126650, 126650, 154276, 173360, 173360, 602136, 602136, 602136, 602447
HTECD88	527214	1944	246 - 356	4631		H0038: 1		
HTECD70	527203	1945	2 - 211	4632	Ala-28 to Ser-43, Ala-57 to Tyr-64.	H0038: 1		
HTECD65	533795	1946	144 - 341	4633		H0038: 1		
HTECD56	527209	1947	3 - 119	4634	Ala-10 to Thr-18.	H0038: 1		
HTECD15	523029	1948	3 - 251	4635	Pro-23 to Val-32, Ala-54 to Ala-60, Thr-68 to Gly-73.	H0038: 1		
HTECC71	508142	1949	3 - 173	4636	Glu-39 to Cys-57.	H0038: 1		
HTECC45	508124	1950	20 - 142	4637	Phe-1 to Gly-10, Leu-32 to Cys-39.	H0038: 1		
HTECC26	508144	1951	74 - 202	4638	Ser-21 to Ser-29, Ala-31 to Thr-37.	H0038: 1		
HTECC09	678659	1952	3 - 365	4639	Arg-1 to Pro-6.	AR089: 39, AR061: 19		



HTECC08	960439	1953						H0038: 1			
HTECA44	508135	1954	2 - 151	4640				H0038: 1			
			56 - 439	4641			Ile-4 to Lys-23, Arg-87 to Cys-103.	H0038: 1			
HTECA39	508132	1955	105 - 236	4642			Gly-9 to Leu-17, Arg-38 to Glu-44.	H0038: 1			
HTEBP54	728811	1956	559 - 744	4643				L0754: 2 and H0038: 1.			
HTEBO43	715704	1957	3 - 266	4644			Gly-42 to Gln-53, Leu-67 to Glu-76.	H0038: 1			
HTEBM87	503275	1958	78 - 230	4645			Glu-16 to Lys-21, Met-25 to Tyr-32.	H0038: 1			
HTEBL53	578544	1959	110 - 367	4646			Pro-7 to Cys-13, Glu-41 to Trp-46, Ser-60 to Gln-65.	H0038: 1			
HTEBJ02	921321	1960	123 - 299	4647				H0038: 1 and L0748: 1.			
HTEBH09	870732	1961	23 - 346	4648			Glu-7 to Gly-14.	H0038: 1 and L0758: 1.			
HTEAX06	960792	1962	134 - 394	4649			Ala-7 to Val-13, Pro-15 to Val-21.	L0758: 3, L0666: 2, L0021: 1, H0038: 1 and L0665: 1.			
HTEAV22	679394	1963	151 - 462	4650				L0439: 2, L0717: 1, H0038: 1, L0769: 1, L0772: 1, L0800: 1, L0666: 1, L0758: 1 and L0601: 1.			
HTEAU39	503295	1964	371 - 144	4651			Ser-8 to Asn-19.	L0439: 4 and H0038: 1.			

HTEAT17	667184	1965	45 - 311	4652			L0758: 5, H0038: 1 and L0768: 1.		
HTEAS02	921323	1966	79 - 324	4653			H0038: 1 and L0758: 1.		
HTEAR93	503298	1967	373 - 230	4654		Ser-19 to Trp-27.	H0038: 1		
HTEAQ55	732562	1968	3 - 398	4655		Asn-14 to Gln-20, Arg-28 to Glu-40.	L0740: 3, L0731: 3, L0748: 2, L0757: 2 and H0038: 1.		
HTEAJ96	503533	1969	216 - 434	4656		Phe-10 to Ser-16, Ser-24 to Gly-50.	H0038: 1		
HTEAH75	503546	1970	145 - 336	4657			H0038: 1		
HTEAG47	503623	1971	146 - 268	4658		Ala-15 to Leu-24, Pro-32 to Cys-41.	L0748: 2 and H0038: 1.		
HTEAG08	960469	1972	17 - 172	4659			H0038: 1 and L0766: 1.		
HTEAB50	724751	1973	7 - 324	4660		Ser-17 to Cys-23, Pro-25 to Ala-32.	H0038: 1 and L0758: 1.		
HTEAA04	925522	1974	106 - 348	4661		Arg-20 to Tyr-28, Phe-31 to Arg-38, Asp-44 to Arg-51.	L0758: 2 and H0038: 1.		
HSWBY36	708291	1975	87 - 218	4662		Arg-17 to Gly-22.	H0546: 1, L0598: 1 and L0759: 1.		
HSWBT69	867537	1976	3 - 380	4663		Ala-26 to Pro-31.	H0546: 1 and L0757: 1.		
HSWBE29	412991	1977	12 - 152	4664		Phe-1 to Asn-9.	H0546: 1 and L0756: 1.		
HSWAS65	953051	1978	15 - 404	4665		Leu-15 to Phe-35, Pro-52 to Ser-58.	H0546: 1	17q21	109270, 109270, 109270,

HSWAS18	666302	1979	200 - 418	4666	Lys-1 to Ser-8.	L0744: 3, L0021: 1, H0546: 1, L0768: 1 and L0657: 1.	109270, 109270, 113705, 113705, 144200, 148065, 148066, 148066, 148067, 148067, 148069, 148080, 154275, 168610, 171190, 176705, 185800, 200350, 221820, 232200, 249000, 252920, 253250, 600119, 600119, 601363, 601844
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HSWAR63	471236	1980	61 - 222	4667	Asn-19 to Asp-30.	H0546: 1	19q13.2	107741, 113900, 122720, 122720, 122720, 126340, 126391, 160900, 164731, 173850, 207750, 248600, 258501
HSWAQ31	697856	1981	194 - 418	4668		H0546: 1		
HPWTA06	936026	1982	71 - 427	4669		H0383: 1 and L0589: 1.		
HPWSA52	727294	1983	155 - 349	4670	Pro-20 to Ser-27.	S0174: 1 and L0755: 1.	6q22.1-q22.3	120110, 121014, 142470, 156225, 164200, 164200, 601316, 601410, 601757
HPWDK45	839559	1984	141 - 533	4671	Lys-9 to Pro-14.	S0044: 1 and L0748: 1.		
HPWDF03	924978	1985	168 - 452	4672		L0749: 4, L0748: 2 and S0044: 1.		
HPWDE86	785710	1986	166 - 291	4673	Cys-13 to Pro-26, Pro-34 to Val-40.	L0754: 2 and S0044: 1.		
HPWCJ90	789170	1987	17 - 397	4674	Cys-1 to Asn-16,	L0731: 2, S0044: 1 and		

							Thr-20 to Asp-44, Ser-47 to Asn-54, Phe-66 to Arg-93.	L0749: 1.		
HPWCG85	638155	1988	461 - 727	4675			Ser-25 to Glu-33, Ser-58 to His-68.	S0044: 1		
	812707	2666	585 - 319	5353			Ser-25 to Glu-33, Ser-58 to His-68.			
HPWBF35	707514	1989	36 - 164	4676			Asn-32 to Thr-40.	S0044: 1 and L0608: 1.		
HPWBE47	720563	1990	251 - 520	4677			Arg-1 to Ile-6, Pro-9 to Met-16, Gly-32 to Arg-37.	S0044: 1 and L0581: 1.		
HPWAT23	676323	1991	73 - 258	4678			Ser-21 to Pro-29, Leu-42 to Ser-52.	S0044: 1 and L0752: 1.		
HPWAJ85	535157	1992	73 - 219	4679			Gln-1 to Gly-11.	S0044: 1 and L0439: 1.		
HPWAJ39	575271	1993	72 - 215	4680				S0044: 1		
HPWAI05	932627	1994	2 - 250	4681			Pro-1 to Pro-9, Ser-36 to Gly-43, Leu-48 to Gln-62.	L0748: 2 and S0044: 1.		
HPWAH19	468246	1995	201 - 1	4682			Pro-13 to Arg-23, Pro-41 to Trp-53, Pro-56 to Lys-65.	S0044: 1		
HPWAG31	867315	2667	27 - 275	5354						
HPVAH71	693618	1996	19 - 165	4683			Arg-28 to Pro-42.	S0044: 1		
HPVAH41	829301	1997	2 - 178	4684				S0013: 1 and L0756: 1.		
	848632	1998	351 - 614	4685			Asp-9 to Phe-18, Pro-44 to Trp-52.	L0748: 2, S0013: 1 and L0743: 1.		
HPVAC74	773298	1999	2 - 637	4686			His-42 to Lys-52.	S0013: 1 and L0740: 1.		
HPVAB16	526124	2000	18 - 155	4687				S0013: 1		
HPVAB01	961017	2001	88 - 261	4688				S0013: 1 and L0746: 1.		

HPRTJ65	753933	2002	391 - 549	4689	Gly-27 to Glu-33, Cys-46 to Lys-53.	H0212: 1, L0750: 1 and L0777: 1.		
HPRTI54	728812	2003	91 - 351	4690		L0605: 2, H0212: 1 and L0748: 1.		
HPRTI16	667652	2004	81 - 470	4691		L0777: 4, H0212: 1, L0809: 1, L0664: 1 and L0750: 1.		
HPRCV66	320393	2005	296 - 472	4692	Ser-1 to Thr-9.	H0032: 1 and L0748: 1.		
HPRCT83	780264	2006	37 - 177	4693		L0731: 2 and H0032: 1.		
HPRCN03	925420	2007	2 - 166	4694		H0032: 1, L0761: 1 and L0758: 1.		
HPRCM12	973740	2008	45 - 278	4695	Lys-11 to Ser-19, Lys-72 to Gln-78.	H0032: 1		
HPRCL72	766311	2009	3 - 248	4696	Lys-4 to Val-12, Ser-23 to Ser-39.	H0032: 1 and L0756: 1.		
HPRCI73	764710	2010	2 - 298	4697		H0032: 1		
HPRCG46	719340	2011	175 - 462	4698	Glu-41 to Ser-46.	H0032: 1 and L0439: 1.		
HPRCD11	967762	2012	2 - 115	4699	Ile-1 to Arg-6; Val-27 to Gly-32.	H0032: 1 and L0748: 1.		
HPRCC22	526623	2013	99 - 236	4700	Arg-6 to Leu-15.	H0032: 1		
HPRCA02	917289	2014	142 - 315	4701	Gln-14 to Tyr-19.	H0032: 1		
	919513	2668	205 - 11	5355	Arg-22 to Asp-27, Gln-36 to Glu-42, Leu-46 to Glu-56.			
HPRBN23	467480	2015	200 - 454	4702	Cys-73 to Lys-82.	H0032: 1		
	486123	2669	484 - 320	5356				

HPRBI87	867409	2670	106 - 282	5357	Met-1 to Asn-9.	H0032: 1 and L0731: 1.	19p13.3-p13.2	108725, 120700, 133171, 136836, 143890, 145981, 147141, 147670, 147670, 147670, 151440, 164953, 188070, 231670, 600276, 600957, 601238, 601843, 601846, 602216, 602477
	695116	2016	93 - 227	4703				
HPRBH80	781636	2017	183 - 344	4704	Ser-21 to Gln-27.	H0032: 1 and L0748: 1.		
HPRAV80	781637	2018	1 - 384	4705		L0439: 3 and H0032: 1.		
HPRAN56	503140	2019	338 - 210	4706	Glu-18 to Val-30.	L0756: 3, L0747: 2, L0749: 2, H0032: 1 and L0748: 1.		
	503152	2671	373 - 543	5358				

HPRAN50	724753	2020	300 - 196	4707		H0032: 1		
HPRAJ75	766496	2021	3 - 197	4708	Ser-19 to Cys-35.	H0032: 1		
HPRAG73	764757	2022	267 - 584	4709		H0032: 1 and L0749: 1.		
HPRAG45	484691	2023	281 - 84	4710	Gly-7 to Thr-27, Pro-60 to Gln-66.	H0032: 1		
	939849	2672	3 - 365	5359	Ile-1 to Ser-8, Ser-103 to Pro-108.			
	939850	2673	1 - 57	5360	Arg-9 to Tyr-14.			
HPRAF86	784594	2024	2 - 232	4711	Thr-13 to Met-23.	H0032: 1		
HPOAB37	789290	2025	2 - 406	4712	Ala-1 to Gln-7.	S0004: 1		
HPMSH94	796839	2026	192 - 368	4713	Lys-13 to Lys-18.	H0111: 1 and L0766: 1.		
HPMSB35	707476	2027	30 - 206	4714		H0111: 1 and L0750: 1.		
HPMMK05	928283	2028	558 - 746	4715	Ser-14 to Arg-19, Glu-43 to Ser-54.	L0754: 2, H0644: 1, L0747: 1 and L0750: 1.		
HPMMB08	957945	2029	105 - 299	4716		H0644: 1 and L0755: 1.		
HPMKP06	933895	2030	3 - 248	4717	Gln-48 to Asp-65.	H0644: 1 and L0777: 1.		
HPMKC05	930874	2031	87 - 257	4718	Asn-8 to Asp-28.	H0644: 1 and L0748: 1.		
HPMJT12	969483	2032	242 - 487	4719	Lys-15 to Leu-25, Met-29 to Leu-43.	L0748: 4 and H0644: 1.		
HPMJN08	958009	2033	2 - 259	4720	His-4 to Arg-20.	H0644: 1 and L0748: 1.		
HPMIK11	965636	2034	277 - 516	4721	Ser-42 to Ser-52.	H0644: 1 and L0462: 1.		



HPMJK03	867615	2035	293 - 436	4722		H0644: 1 and L0700: 1.		
HPMJ11	965627	2036	61 - 381	4723	Gln-7 to Gly-18, Asp-21 to Met-28.	H0644: 1 and L0774: 1.		
HPMJE06	939682	2037	169 - 2	4724	Tyr-39 to Arg-56.	H0644: 1, L0606: 1 and L0749: 1.		
HPMJA11	965628	2038	1 - 327	4725		L0745: 4 and H0644: 1.		
HPMGX92	491004	2039	346 - 158	4726	Glu-36 to Ala-43, Pro-45 to Lys-57.	H0031: 1		
	881472	2674	63 - 350	5361	Leu-20 to Arg-26, Ala-38 to Thr-43, Trp-90 to Ala-96.			
HPMGR15	660374	2040	178 - 378	4727	Pro-18 to Glu-24.	H0031: 1 and L0756: 1.		
HPMGO88	463906	2041	267 - 440	4728		H0031: 1 and L0756: 1.		
HPMGM39	705460	2042	865 - 1128	4729	Thr-1 to Ser-6, Glu-49 to Phe-63.	L0748: 6, H0031: 1, L0747: 1, L0756: 1 and L0596: 1.		
	662021	2043	85 - 195	4730	Lys-28 to Ser-33.	H0031: 1		
HPMGD63	694518	2044	177 - 380	4731	Gln-6 to Gly-11, Phe-21 to Thr-30, Arg-50 to Thr-63.	H0031: 1 and L0748: 1.		
	690704	2045	6 - 161	4732		L0747: 2 and H0031: 1.		
HPMFL73	867670	2046	203 - 592	4733		H0031: 1		
HPMFC02	920327	2047	112 - 576	4734	Pro-41 to Ala-63, Gly-69 to Gly-81.	L0770: 2, L0779: 2, H0031: 1, L0766: 1,		

HPMFB26	867674	2048	2 - 361	4735	Gly-4 to His-11, Val-61 to Gly-67.	L0776: 1 and L0758: 1.		
HPMEG77	772503	2049	214 - 366	4736	Leu-21 to Val-36, Pro-38 to Gln-44.	H0031: 1 and L0747: 1.		
HPMDQ89	880787	2050	1 - 390	4737	Arg-1 to Phe-9, Arg-69 to Gln-83, Lys-85 to Leu-103, Val-117 to His-122.	L0604: 3 and H0031: 1.		
HPMDP10	968350	2051	1 - 258	4738	Gly-1 to Gln-7, Gly-21 to Val-26, Arg-47 to Arg-55, Lys-71 to Ala-77.	L0794: 2 and H0031: 1.		
HPMDF06	954567	2052	1 - 111	4739		L0794: 2, H0031: 1 and L0779: 1.		
HPMAM93	791407	2053	150 - 1	4740	Lys-42 to Ile-50.	H0031: 1 and L0455: 1.		
HPMAL77	772740	2054	629 - 426	4741		L0439: 2 and H0031: 1.		
HPMAL73	764752	2055	2 - 169	4742	Ser-2 to Tyr-15.	L0748: 3, H0031: 1 and L0731: 1.		
HPMAK71	503690	2056	323 - 442	4743	Leu-7 to Leu-12, Asn-14 to His-27, Pro-30 to Lys-37.	H0031: 1 and L0745: 1.		
HPMAJ83	781518	2057	156 - 410	4744		H0031: 1		
HPMAJ80	572808	2058	2 - 154	4745	Arg-27 to Thr-46.	H0031: 1 and L0748: 1.		
HPMAJ10	968695	2059	215 - 63	4746		H0031: 1		
HPMAH85	783344	2060	84 - 233	4747	Lys-1 to Lys-8.	H0031: 1 and L0740: 1.		

HPMAH56	867711	2061	156 - 296	4748			1.			
HPMAB10	968723	2062	3 - 221	4749	Pro-3 to Gly-11, Ser-43 to Leu-55.		H0031: 1			
HPLBW22	679217	2063	3 - 278	4750	Glu-8 to His-17, Gln-19 to Gly-43, Thr-62 to Ser-73, Pro-80 to Leu-85.		H0031: 1 and L0758: 1.			
HPLBW02	921331	2064	338 - 499	4751			H0030: 1 and L0595: 1.			
HPLBT54	731065	2065	179 - 343	4752	Pro-1 to Ala-12, Gly-33 to Gln-38.		L0777: 2 and H0030: 1.			
HPLBT53	728517	2066	283 - 450	4753	Ile-36 to Gly-47.		H0030: 1 and L0754: 1.			
HPLBS41	712707	2067	359 - 559	4754	Pro-16 to Ser-23.		H0030: 1 and L0758: 1.			
HPLBQ96	796069	2068	18 - 155	4755	Lys-6 to Asn-12.		L0747: 2 and H0030: 1.			
HPLBO90	787208	2069	202 - 348	4756	Leu-30 to Cys-39.		H0030: 1 and L0754: 1.			
HPLBN79	781854	2070	144 - 326	4757	Glu-4 to Arg-9, Thr-17 to Lys-23.		H0030: 1 and L0751: 1.			
HPLBB47	975477	2071	745 - 491	4758	Lys-22 to Ser-39.		H0030: 1 and L0756: 1.			
HPLAX14	727885	2072	85 - 489	4759	Ser-7 to Gly-15, Pro-66 to Trp-73, Thr-96 to Gly-101, Gly-109 to Arg-133.		L0518: 2, H0030: 1 and L0740: 1.			
HPLAV44	715732	2073	197 - 3	4760	His-23 to Asn-37.		H0030: 1, L0747: 1 and L0750: 1.			
							H0030: 1 and L0748: 1.			

HPLAI10	968707	2074	54 - 461	4761	Ser-14 to Phe-20.	1. H0030: 1, L0517: 1, L0740: 1, L0754: 1, L0777: 1, L0755: 1 and L0758: 1.		
	968711	2675	659 - 372	5362	Leu-3 to Lys-8, Arg-27 to Ser-34, Leu-45 to Lys-55.			
HPJFA10	963322	2075	466 - 341	4762	Gln-9 to Ala-15.	L0783: 1, L0809: 1 and S0152: 1.		
HPJEV95	929723	2076	82 - 408	4763		AR061: 4, AR089: 1 S0152: 1 and L0601: 1.		
HPJEU01	928408	2077	209 - 352	4764		S0152: 1 and L0439: 1.		
HPJET11	963894	2078	136 - 327	4765	Lys-35 to Lys-42.	L0717: 1, S0152: 1 and L0756: 1.		
HPJES17	859867	2079	19 - 318	4766	Glu-8 to Cys-16.	L0435: 1, S0152: 1, L0439: 1 and L0747: 1.		
HPJEL02	918315	2080	50 - 220	4767	Pro-26 to Phe-35.	S0152: 1 and L0745: 1.		
HPJEG53	974074	2081	19 - 198	4768		S0152: 1		
HPJDW93	867759	2082	44 - 406	4769		S0152: 1 and L0604: 1.		
HPJDT03	922815	2083	177 - 392	4770		S0152: 1 and L0759: 1.		
HPJDP54	949149	2084	155 - 301	4771		L0532: 1 and S0152: 1.		
HPJDF61	889928	2085	280 - 417	4772		AR054: 38, AR051: 29, AR050: 28 S0152: 1		
HPJDC01	915056	2086	212 - 358	4773	Asn-17 to Met-22.	S0152: 1 and L0779: 1.		
HPJDA25	951281	2087	246 - 506	4774	Gln-1 to Cys-17, Gln-20 to Lys-28, Pro-35 to Ser-44.	AR061: 6, AR089: 2 S0152: 1		

	951284	2676	252 - 13	5363			
HPJCU29	928407	2088	1 - 195	4775		L0667: 1 and S0152: 1.	
HPJCT81	494874	2089	148 - 396	4776	Thr-2 to Asn-8, Asn-49 to Ser-54.	S0152: 1 and L0605: 1.	
HPJCT26	559949	2090	210 - 635	4777	Arg-1 to Gly-7.	AR054: 34 S0152: 1	
HPJCS73	975087	2091	3 - 227	4778	Ser-33 to Lys-41.	S0152: 1	
HPJCS43	715082	2092	62 - 322	4779	Pro-10 to Ser-17, Ser-19 to Arg-24, Pro-43 to Glu-50, Arg-56 to Phe-64, Pro-74 to His-87.	S0152: 1	
HPJCS32	699046	2093	179 - 274	4780	Val-23 to Leu-31.	S0152: 1	
HPJCN60	887600	2094	1 - 210	4781	Ile-20 to Trp-33, Thr-35 to Gly-45.	AR051: 17, AR050: 9, AR054: 8 S0152: 1	
HPJCL55	670083	2095	458 - 291	4782	Glu-11 to His-16.	L0758: 3, L0779: 2 and S0152: 1.	
HPJBU40	710928	2096	137 - 373	4783		L0748: 2 and S0152: 1.	
HPJBU09	625362	2097	3 - 182	4784	Arg-14 to Cys-22.	L0439: 2 and S0152: 1.	
HPJBS74	765390	2098	310 - 591	4785		S0152: 1 and L0592: 1.	
HPJBS52	726535	2099	141 - 518	4786	Phe-2 to Asp-8.	S0152: 1 and L0743: 1.	
HPJBS35	867818	2100	64 - 249	4787		S0152: 1 and L0748: 1.	
HPJBL76	769889	2101	340 - 546	4788		S0152: 1, L0740: 1 and L0750: 1.	
HPJBL30	948721	2102	354 - 145	4789	Tyr-10 to Leu-15, Glu-32 to Gly-41.	L0752: 7, L0780: 2, L0586: 1 and S0152: 1.	
HPJBK25	974606	2103	17 - 154	4790	His-15 to Gln-26, Ser-38 to Asn-46	S0152: 1	

HPJBK14	974593	2104	2 - 331	4791	Pro-8 to Leu-18, Gly-45 to Ala-53, Pro-56 to Trp-63, Pro-67 to Arg-73.	S0152: 1		
HPJBH45	717088	2105	252 - 404	4792	Ser-7 to Lys-12.	L0754: 2 and S0152: 1.		
HPJAX30	607408	2106	762 - 544	4793		S0152: 1		
	884685	2677	104 - 370	5364	Ser-41 to Trp-46, Cys-57 to Gln-68, Tyr-79 to Gly-84.			
	885717	2678	643 - 1290	5365				
HPJAU73	806718	2107	170 - 319	4794		S0152: 1 and L0748: 1.		
HPJAP92	887830	2108	164 - 322	4795		AR050: 26, AR051: 20, AR054: 10 S0152: 1		
HPJAO13	824243	2109	716 - 531	4796	Ser-2 to Arg-7.	AR061: 2, AR089: 1 S0152: 1		
	892302	2679	865 - 1110	5366	Gln-10 to Leu-26.			
	945194	2680	127 - 612	5367				
HPJAN69	754858	2110	79 - 360	4797	Pro-75 to Phe-84.	S0152: 1		
HPJAN67	751384	2111	3 - 176	4798		S0152: 1		
HPJAN57	734503	2112	65 - 166	4799		S0152: 1		
HPJAJ20	669000	2113	476 - 652	4800	Thr-31 to Glu-37.	S0152: 1 and L0439: 1.		
HPJAE51	725761	2114	193 - 2	4801	Ser-42 to Lys-48.	L0439: 2 and S0152: 1.		
HPJAA27	419786	2115	3 - 278	4802	Leu-17 to Asn-31, Gly-55 to Ala-62, Arg-66 to Ala-87.	S0152: 1 1q32.1	134580, 145260, 600105, 600759, 601975	
HPICG93	887817	2116	20 - 310	4803	Leu-62 to Ser-75.	AR051: 32, AR050:		

							26, AR054: 17 S0150: 1			
HPICE06	935095	2117	607 - 816	4804			S0150: 1, L0439: 1 and L0740: 1.			
HPIBY36	708183	2118	296 - 517	4805			L0439: 2, L0756: 2, S0150: 1 and L0438: 1.			
HPIBT62	743135	2119	123 - 362	4806			S0150: 1, L0748: 1 and L0439: 1.			
HPIBO89	786741	2120	213 - 473	4807		Lys-79 to Phe-85.	L0439: 3, S0150: 1, L0740: 1 and L0749: 1.			
HPIBI89	867845	2121	1 - 135	4808		Glu-7 to Ser-13.	S0150: 1 and L0748: 1.			
HPIBH31	838809	2122	169 - 420	4809		Val-3 to Gly-14, Ser-65 to Gly-72.	S0150: 1 and L0748: 1. 2p22-p21		120435, 120435, 126600, 135300, 136435, 152790, 152790, 157170, 182601, 278300, 601071, 601771, 602134	
HPIBC93	785971	2123	1 - 285	4810		Ser-49 to Pro-54, Pro-60 to His-70.	S0150: 1 and L0751: 1.			
HPIBB45	867850	2124	77 - 178	4811			S0150: 1			
HPIBB43	715037	2125	47 - 247	4812			S0150: 1			
HPIBB32	698901	2126	1 - 186	4813			S0150: 1			
HPIBB19	668489	2127	182 - 289	4814			S0150: 1			

HP1AW91	790033	2128	223 - 426	4815	Ala-6 to Ser-25.	L0748: 2 and S0150: 1.		
HP1AV06	935111	2129	41 - 322	4816	Cys-19 to Trp-24, Ser-29 to Glu-34, Phe-47 to Trp-52, Arg-57 to Gly-68.	L0717: 2 and S0150: 1.		
HP1AQ70	973604	2130	185 - 436	4817	Gly-36 to Thr-41.	AR089: 18, AR061: 9 S0150: 1		
HP1AP79	774817	2131	102 - 476	4818	Asp-7 to Thr-15.	L0439: 6 and S0150: 1.		
HP1AD10	906987	2132	547 - 834	4819	Lys-91 to Pro-96.	S0150: 1 and L0365: 1.		
	961313	2681	172 - 35	5368				
HPHBSB91	790313	2133	157 - 273	4820	Val-33 to Lys-39.	S0176: 1		
HPHBSB21	671118	2134	52 - 189	4821		S0176: 1		
HPHSA94	793084	2135	3 - 209	4822		S0176: 1		
HPHAE81	778036	2136	417 - 127	4823		S0148: 1 and L0748: 1. 19q13.1	164731, 172400, 172400, 180901, 180901, 221770, 248600, 600918, 602716	
HPFMG06	933696	2137	1 - 120	4824		H0674: 1 and L0362: 1.		
HPFMB10	961758	2138	414 - 683	4825	Lys-2 to Lys-10.	H0674: 1 and L0363: 1.		
HPFDX38	709302	2139	398 - 583	4826		H0169: 1 and L0766: 1.		
HPFCZ82	780198	2140	3 - 341	4827	Pro-108 to Gly-113.	H0169: 1 and L0747:		



HPFCZ60	430125	2141	298 - 444	4828			1. H0169: 1 and L0740: 1.		
HPFCZ10	968360	2142	33 - 272	4829			H0169: 1		
HPFCR23	675120	2143	93 - 263	4830		Thr-52 to Tyr-57.	H0169: 1, L0809: 1 and L0754: 1.		
HPFCP82	867881	2144	435 - 632	4831		Pro-24 to Gly-44, Pro-47 to Tyr-56.	AR050: 7, AR054: 3, AR051: 1 H0169: 1		
HPFCP53	526574	2145	138 - 245	4832			AR050: 20, AR051: 4, AR054: 4 H0169: 1		
HPFCM45	723501	2146	72 - 251	4833			H0169: 1, L0766: 1, L0776: 1, L0790: 1, L0741: 1 and L0779: 1.		
HPFCM27	682098	2147	178 - 294	4834			L0598: 2, H0169: 1 and L0731: 1.		
HPFCL56	732601	2148	20 - 187	4835		Cys-6 to His-17.	H0169: 1 and L0777: 1.		
HPFCL24	867889	2149	56 - 274	4836			L0752: 2, H0169: 1, L0794: 1 and L0751: 1.		
HPFCG02	921196	2150	94 - 261	4837		Gly-33 to Arg-39.	H0169: 1 and L0748: 1.		
HPFCA01	928672	2151	151 - 393	4838		Gly-18 to His-30.	L0748: 2 and H0169: 1.		
HPELD12	969248	2152	231 - 623	4839		Gly-18 to Glu-29, Leu-55 to Gln-60, His-109 to Gly-117, Gly-122 to Pro-127.	H0673: 1, L0805: 1 and L0731: 1.		

HPEKI04	926104	2153	43 - 165	4840			L0748: 2, H0673: 1 and L0749: 1.		
HPEKE01	914414	2154	159 - 350	4841			H0673: 1, L0769: 1 and L0768: 1.		
HPEBT82	524246	2155	1 - 111	4842			H0166: 1		
HPEBT78	773844	2156	59 - 148	4843		Lys-15 to Gly-25.	H0166: 1		
HPEBT68	753692	2157	45 - 245	4844		Lys-9 to Trp-17.	H0166: 1		
HPEBT54	731002	2158	86 - 397	4845		Lys-26 to Cys-31, Arg-38 to Asp-46.	H0166: 1		
HPEBT49	530021	2159	106 - 300	4846		Leu-12 to Ser-17.	H0166: 1		
HPEBT34	706836	2160	44 - 301	4847		Asp-20 to His-27.	H0166: 1		
HPEBT14	535061	2161	3 - 98	4848			H0166: 1		
HPEBT07	954214	2162	42 - 317	4849		Thr-78 to Arg-84.	H0166: 1		
HPEBO67	578516	2163	1 - 228	4850		Glu-12 to Thr-39.	H0166: 1, L0748: 1 and L0747: 1.		
HPEBL08	960240	2164	227 - 313	4851		Lys-19 to Asn-27.	L0770: 2, H0166: 1, L0665: 1 and L0749: 1.		
HPEBH01	921767	2165	105 - 341	4852			H0166: 1 and L0745: 1.		
HPEBG89	785942	2166	80 - 277	4853		Gly-2 to Cys-7, Glu-28 to Glu-40, Glu-53 to Lys-58.	L0759: 2 and H0166: 1.		
HPEBG10	867888	2167	75 - 284	4854		Phe-26 to Trp-32.	H0166: 1 and L0542: 1.		
HPEBA89	910250	2168	268 - 504	4855		Cys-14 to Ser-26, Glu-40 to Lys-58.	AR061: 57, AR089: 38 H0166: 1 and L0749: 1.		
	912272	2682	182 - 361	5369		Cys-14 to Ser-26, Glu-40 to Lys-60.			

HPEBA61	742251	2169	2 - 70	4856			H0166: 1		
HPEBA05	928027	2170	2 - 178	4857	Gly-14 to Ser-19.		H0166: 1 and L0779: 1.		
HPEAG43	468542	2171	83 - 232	4858			H0165: 1		
	589933	2683	776 - 1117	5370	Pro-4 to Thr-17.				
HPEAD72	761472	2172	45 - 383	4859			H0165: 1 and L0744: 1.		
HPEAB12	968847	2173	2 - 178	4860	Ser-7 to Lys-13, Leu-29 to Ser-36.		L0794: 4 and H0165: 1.		
HPEAA57	514231	2174	199 - 414	4861	Leu-11 to Ala-18, Gly-22 to Ser-41.		H0165: 1		
HPEAA40	867899	2175	186 - 308	4862			H0165: 1 and L0526: 1.		
HPDWR11	965249	2176	261 - 548	4863	Gly-1 to Thr-13, Arg-37 to Ser-45, Arg-52 to Asn-73.		L0759: 2, L0769: 1, L0768: 1, L0794: 1, L0805: 1, H0658: 1, L0750: 1 and L0777: 1.		
	928563	2177	287 - 472	4864			L0439: 2, L0717: 1, L0803: 1, H0658: 1 and L0777: 1.		
HPDVM01	913859	2178	311 - 433	4865			L0779: 2 and H0658: 1.		
HPDVD11	965276	2179	25 - 117	4866	Ala-10 to Lys-18.		H0658: 1 and L0779: 1.		
HPDRU11	965307	2180	118 - 342	4867	Gly-13 to Trp-21.		H0658: 1 and L0756: 1.		
HPDRR06	968601	2181	448 - 74	4868	Pro-65 to His-76, Asn-110 to Phe-118.		L0666: 2, L0766: 1, L0655: 1 and H0658: 1.		
HPDRN07	951838	2182	54 - 299	4869	Asp-11 to Asn-17.		H0658: 1 and L0604: 1.		

HPDRG01	914416	2183	339 - 674	4870			1. L0748: 2, H0658: 1 and L0750: 1.			
HPDPS12	969342	2184	1 - 255	4871	Arg-10 to Gln-16, Pro-24 to Gly-30.		H0658: 1, L0777: 1 and L0592: 1.			
HPDPP12	969341	2185	3 - 179	4872	Thr-1 to Asn-13, Pro-35 to Lys-42.		L0523: 1 and H0658: 1.			
HPDPC08	957822	2186	120 - 398	4873	Arg-23 to Val-29.		H0658: 1	13		
HPDOW10	961782	2187	280 - 429	4874	Met-6 to His-12.		L0766: 2, L0776: 2, H0658: 1 and L0779: 1.			
HPDOO10	961881	2188	338 - 520	4875			L0769: 3 and H0658: 1.			
HPDOF11	965491	2189	30 - 227	4876			L0770: 2 and H0658: 1.			
HPCTK02	917480	2190	207 - 446	4877			H0659: 1, L0740: 1 and L0756: 1.			
HPCTD03	922149	2191	3 - 332	4878			AR089: 6, AR061: 2 H0659: 1			
HPCTC04	925777	2192	150 - 347	4879	Arg-40 to Gln-47.		L0659: 2, H0659: 1 and L0779: 1.			
HPCQQ07	951646	2193	2 - 328	4880	Arg-6 to Arg-11.		L0805: 1, L0776: 1 and H0659: 1.			
HPCPM63	954940	2194	85 - 222	4881			L0800: 1, H0659: 1 and L0747: 1.			
HPCOV68	911075	2195	97 - 249	4882			AR089: 23, AR061: 7 L0439: 2, L0369: 1 and H0659: 1.			
HPCAO89	946913	2196	1 - 369	4883	Pro-18 to Gln-28, Gln-42 to Asn-49,		AR050: 18, AR054: 18, AR089: 5, AR051:			

					Ser-72 to Arg-81.	4, AR061: 2 L0761: 1 and S0146: 1.			
HPCAK66	320415	2197	85 - 237	4884	Lys-9 to Tyr-14, Glu-44 to His-50.	S0146: 1			
HPCAG81	778177	2198	190 - 348	4885		S0146: 1 and L0754: 1.			
HPCAF65	573368	2199	75 - 275	4886	Asp-38 to Ala-43.	S0146: 1			
HPCAD17	584754	2200	465 - 271	4887	Glu-16 to Glu-27, Glu-35 to Ser-46, Glu-56 to Ala-64.	S0146: 1			
	584755	2684	145 - 312	5371					
HPCAB54	728857	2201	2 - 409	4888	Gly-1 to Gly-11.	S0146: 1 and L0591: 1.			
HPCAB45	575233	2202	8 - 247	4889	Pro-21 to Thr-40.	S0146: 1			
HOVEV01	914553	2203	49 - 540	4890	Gly-50 to Thr-57, Gln-60 to Trp-74, Glu-86 to Cys-96, Met-106 to Gly-124.	L0748: 3, L0603: 2, H0428: 1, L0771: 1, L0749: 1 and L0757: 1.			
HOVEU10	961865	2204	170 - 328	4891		H0428: 1			
HOVEU06	933737	2205	106 - 201	4892		H0428: 1			
HOVEO04	926209	2206	18 - 179	4893	Ser-27 to Gly-32.	H0428: 1 and L0750: 1.			
HOVEE20	909030	2207	88 - 444	4894	Asn-7 to Met-12, Cys-38 to Thr-44.	AR089: 7, AR061: 2 H0428: 1			
HOVDD82	948619	2208	2 - 172	4895	Arg-2 to Cys-11, Cys-15 to Gly-20.	H0428: 1 and L0766: 1.			
HOVDD10	961887	2209	3 - 323	4896	Glu-25 to Pro-39, Thr-44 to Tyr-50, Pro-53 to Gln-60, Ser-67 to Val-82.	H0428: 1 and L0462: 1.			
HOVCP77	772210	2210	120 - 299	4897	Tyr-17 to Gln-23,	L0439: 12 and H0428:			

HOVCO50	932544	2211	425 - 586	4898	Lys-32 to Ser-38.	1. H0428: 1, L0752: 1 and L0759: 1.		
HOVCN57	734779	2212	143 - 301	4899	Lys-1 to Gln-12, Cys-44 to Lys-49.	H0428: 1 and L0744: 1.		
HOVCM77	772208	2213	107 - 265	4900	Arg-30 to Lys-39.	H0428: 1 and L0439: 1.		
HOVCM03	924196	2214	159 - 257	4901	Glu-10 to Thr-18.	H0428: 1 and L0750: 1.		
HOVCI89	786917	2215	194 - 322	4902		H0428: 1		
HOVCI08	959470	2216	938 - 75	4903	Pro-43 to Ser-49.	H0428: 1, L0743: 1, L0744: 1, L0747: 1, L0752: 1 and L0592: 1.		
HOVCD33	702445	2217	124 - 252	4904	Asp-33 to Val-38.	L0439: 2 and H0428: 1.		
HOVCC57	465313	2218	210 - 380	4905		H0428: 1 and L0581: 1.		
HOVBQ07	858863	2219	200 - 604	4906	Asp-1 to Val-13, Ser-17 to Ser-26.	H0428: 1, L0764: 1 and L0758: 1.		
HOVBK69	757594	2220	116 - 424	4907		H0428: 1 and L0740: 1.		
HOVBK38	956238	2221	33 - 263	4908		L0766: 2, H0428: 1, L0775: 1, L0782: 1, L0783: 1, L0748: 1 and L0758: 1.		
HOVBK24	858857	2222	75 - 353	4909	Gln-1 to Leu-7, Ser-32 to His-42.	H0428: 1, L0748: 1 and L0581: 1.		
HOVBI67	751665	2223	155 - 355	4910		L0749: 2 and H0428: 1.		

HOVBI20	669730	2224	1 - 183	4911		H0428: 1 and L0748: 1.		
HOVAZ89	904818	2225	2 - 298	4912	Glu-14 to Pro-19, Arg-24 to Arg-36, Arg-85 to His-90.	H0428: 1		
HOVAZ65	750273	2226	275 - 457	4913		L0740: 2 and H0428: 1.		
HOVAY88	827077	2227	203 - 409	4914	Asn-20 to Lys-25.	H0428: 1		
HOVAY58	736077	2228	179 - 388	4915	Val-1 to Thr-11, Tyr-23 to Leu-31, Arg-47 to Thr-52.	H0428: 1 and L0754: 1.		
HOVAY42	713812	2229	168 - 320	4916	Asn-20 to Glu-26.	H0428: 1		
HOVAY03	921959	2230	147 - 1	4917		H0428: 1		
HOVAW62	745704	2231	2 - 247	4918		L0516: 2, H0428: 1 and L0753: 1.		
HOVAO25	678163	2232	112 - 270	4919		H0428: 1 and L0748: 1.		
HOVAN51	725005	2233	3 - 122	4920		L0748: 5, H0428: 1 and L0749: 1.		
HOVAJ07	953422	2234	279 - 452	4921	Lys-40 to Phe-47.	H0428: 1 and L0743: 1.		
HOVAI05	932093	2235	2 - 199	4922	Val-41 to Lys-46.	H0428: 1 and L0752: 1.		
HOVAF07	953553	2236	22 - 102	4923		H0428: 1		
HOVAF01	916770	2237	245 - 3	4924	Phe-58 to Arg-67, Leu-71 to Thr-77.	H0428: 1		
HOVAC77	578783	2238	181 - 366	4925		H0428: 1		
HOVAC54	578809	2239	36 - 197	4926	Ile-23 to Cys-35.	H0428: 1 and L0748: 1.		

HOVAC26	578810	2240	45 - 278	4927	Gln-12 to Gly-17, Ser-28 to Pro-39.	H0428: 1		
HOVAB85	578788	2241	3 - 407	4928	Asp-1 to Arg-6, Thr-31 to Leu-43, Val-53 to His-59, Pro-61 to Val-73, Ser-81 to Ser-96.	H0428: 1		
HOVAB61	578791	2242	256 - 477	4929		L0756: 2, L0361: 2, H0428: 1, L0598: 1 and L0592: 1.		
HOOKF10	961499	2243	210 - 359	4930	Lys-38 to Lys-50.	L0776: 1 and H0648: 1.		
HOOKF04	925784	2244	508 - 239	4931	Thr-31 to Lys-40.	L0758: 3, L0779: 2, H0648: 1 and L0740: 1.		
HOOU04	925774	2245	17 - 283	4932		H0648: 1 and L0777: 1.		
HOON04	925783	2246	3 - 260	4933	Arg-21 to Leu-27.	L0770: 1, L0794: 1, L0804: 1 and H0648: 1.		
HOOK11	965292	2247	205 - 420	4934	Pro-48 to Phe-72.	H0648: 1 and L0750: 1.		
HOONH05	928627	2248	37 - 210	4935	Val-16 to Thr-26, Pro-30 to Ser-36, Pro-53 to Glu-58.	L0758: 3 and H0648: 1.		
HOONJ02	917454	2249	248 - 379	4936	Lys-34 to Gly-41.	H0648: 1 and L0758: 1.		
HOONL05	928644	2250	280 - 444	4937	Pro-42 to Asp-55.	L0751: 3, L0764: 1, L0518: 1, H0648: 1, L0747: 1 and L0752: 1.		
HOONIG03	922510	2251	2 - 205	4938	Glu-34 to Glu-44.	H0648: 1 and L0596: 1.		



HOOHP02	917424	2252	210 - 374	4939	Phe-13 to Gln-24.	H0648: 1, L0748: 1, L0751: 1, L0754: 1 and L0749: 1.		
HOOHE67	969061	2253	1 - 171	4940		H0648: 1, L0754: 1 and L0750: 1.		
HOOHD06	933873	2254	1 - 150	4941	Arg-1 to Cys-10, Lys-17 to Gly-24.	L0666: 1 and H0648: 1.		
HOOAB23	522227	2255	249 - 49	4942	His-1 to Gln-7, Gly-14 to Gly-23, Leu-50 to Arg-67.	H0028: 1 and L0792: 1.		
HOOAB05	932925	2256	196 - 579	4943	Ser-66 to Pro-76.	H0028: 1 and L0777: 1.		
HONAK10	968610	2257	3 - 116	4944	Glu-1 to Lys-6.	L0766: 1 and T0068: 1.		
HONAH06	936029	2258	677 - 333	4945		AR051: 655, AR050: 494, AR054: 346 T0068: 1		
HONAE50	723571	2259	344 - 559	4946	Gly-18 to Thr-32.	T0068: 1 and L0749: 1.		
HONAD65	747152	2260	174 - 290	4947	Ser-6 to Lys-14.	T0068: 1 and L0592: 1.		
HONAD02	859016	2261	732 - 1040	4948		AR061: 1, AR089: 1 T0068: 1 and L0779: 1.		
HOGEW23	973221	2262	2 - 145	4949	Ser-1 to Gly-11.	H0435: 1		
HOGDQ03	922578	2263	163 - 414	4950		L0774: 1 and H0435: 1.		
HOGCW89	973227	2264	484 - 732	4951	Lys-10 to Asn-16.	H0435: 1		
HOGCT13	657284	2265	389 - 763	4952		L0439: 2 and H0435: 1.		
HOGCR31	463874	2266	205 - 441	4953		H0435: 1 and L0743: 1.		
HOGCR10	964761	2267	1 - 240	4954		H0435: 1 and L0748: 1.		

HOGCQ54	859076	2268	3 - 608	4955	Ser-19 to Asp-31.	1.	L0766: 3 and H0435:		
HOGCH05	930813	2269	2 - 202	4956		1.	H0435: 1 and L0748:	9q31.2	223900, 253800, 253800
HOGCE07	859077	2270	126 - 509	4957		1.	L0369: 1 and H0435:		
HOGCD61	761991	2271	247 - 393	4958			H0435: 1		
HOGCC63	745130	2272	101 - 241	4959	Gly-2 to Tyr-8.	1.	L0745: 2 and H0435:		
HOGCA65	750308	2273	298 - 501	4960	Arg-8 to Leu-17.	1.	L0748: 2 and H0435:		
HOGBJ26	847191	2274	208 - 50	4961	Ser-17 to Trp-23.	1.	H0435: 1 and L0439:		
HOGBE27	682232	2275	2 - 163	4962	Arg-1 to Phe-13.	1.	H0435: 1 and L0747:		
HOGAM56	908904	2276	973 - 779	4963			H0435: 1		
HOGAI73	764490	2277	227 - 379	4964	Lys-3 to Phe-8.	1.	H0435: 1 and L0777:		
HOGAI26	681919	2278	221 - 397	4965	Arg-1 to Gly-19, Lys-35 to Trp-43.	1.	L0748: 2 and H0435:		
HOGAH71	760431	2279	163 - 369	4966	Asp-22 to His-28, Arg-49 to Ser-54.	1.	H0435: 1 and L0596:		
HOGAG57	734848	2280	2 - 634	4967	Lys-10 to Ser-15, Arg-44 to Ser-62, Glu-78 to Thr-83, Lys-115 to Phe-124, Glu-137 to Asp-148,		L0747: 2, H0435: 1, L0742: 1, L0596: 1 and L0591: 1.		

HOGAD77	772319	2281	298 - 576	4968	Gly-165 to His-171, Glu-189 to Lys-211.	L0748: 2 and H0435: 1.		
HOGAC69	756713	2282	578 - 324	4969		H0435: 1		
HOFNW81	789232	2283	46 - 336	4970	Asp-48 to Glu-53, Pro-72 to Ser-81.	H0415: 1		
HOFNW69	533713	2284	213 - 28	4971	Glu-17 to His-23, His-26 to Ser-34, Gly-40 to Glu-45.	H0415: 1	1q21	104770, 107670, 110700, 135940, 145001, 146790, 152445, 152445, 159001, 174000, 179755, 182860, 182860, 182860, 191315, 230800, 230800, 266200, 600897, 601105, 601412, 601652, 602491

HOFNW68	753048	2285	1 - 132	4972	Lys-18 to Asp-23.	H0415: 1		
HOFNW65	815822	2286	3 - 431	4973	Arg-14 to Asn-19, Ala-35 to Ser-45, Gln-74 to Glu-90.	AR089: 5, AR061: 3 H0415: 1		
HOFNW45	720755	2287	2 - 118	4974	Asn-12 to Glu-19, Lys-30 to Phe-35.	H0415: 1		
HOFNW07	953436	2288	37 - 411	4975	Arg-10 to Arg-19, Asn-50 to Ser-61, Met-65 to Lys-71, Ala-83 to Asn-89.	H0415: 1		
HOFNU50	724437	2289	3 - 347	4976	Phe-5 to Pro-10, Gln-71 to Ser-77, Lys-86 to Glu-91.	L0748: 2 and H0415: 1.		
HOFNL96	888569	2290	3 - 380	4977	Pro-3 to Ala-17, Asn-56 to Asp-62, Gln-85 to Gly-100.	H0415: 1		
HOFNI90	788947	2291	90 - 323	4978	Gln-1 to Ser-6, Ser-36 to Ser-45, Leu-47 to Pro-54, Arg-59 to Gly-69.	H0415: 1		
HOFNI85	784366	2292	1 - 138	4979		H0415: 1		
HOFNI72	760643	2293	52 - 273	4980		H0415: 1		
HOFNI71	760392	2294	59 - 253	4981	Arg-1 to Arg-6.	H0415: 1		
	773729	2685	1 - 177	5372	Gly-9 to His-30, Arg-48 to Pro-57.			
HOFNI58	859094	2295	151 - 351	4982		H0415: 1		
HOFNI56	859093	2296	166 - 408	4983	Gln-7 to Gly-15.	H0415: 1		
HOFNI42	713816	2297	111 - 302	4984		H0415: 1		
HOFNI37	859102	2298	35 - 232	4985		H0415: 1		

HOFNI33	859103	2299	3 - 263	4986			H0415: 1		
HOFNI32	699299	2300	2 - 217	4987	Gly-1 to Gly-11, Thr-59 to Gly-64.		H0415: 1		
HOFNI10	964682	2301	2 - 193	4988			H0415: 1		
HOFNI02	917347	2302	1 - 201	4989	Gln-16 to Gln-23.		H0415: 1		
HOFNC80	835718	2303	1 - 315	4990	Ser-9 to Lys-18.		AR051: 12, AR050: 12, AR054: 10, AR061: 2, AR089: 1		
							H0415: 1		
HOFNC79	774037	2304	139 - 243	4991	Glu-21 to Asp-26.		H0415: 1		
HOFNB63	613681	2305	179 - 3	4992			H0415: 1		
HOFNB55	731801	2306	2 - 67	4993	Arg-1 to Thr-15.		H0415: 1		
HOFNB51	725684	2307	187 - 432	4994	Arg-18 to Lys-24.		H0415: 1		
HOFMU70	489858	2308	2 - 154	4995	Arg-18 to Gly-24.		H0415: 1		
HOFMU67	743184	2309	256 - 528	4996	Gln-85 to Pro-91.		H0415: 1		
HOFMU29	824242	2310	993 - 625	4997			H0415: 1		
	902061	2686	217 - 402	5373					
HOFMT55	888552	2311	87 - 239	4998	Val-17 to Glu-24.		AR050: 84, AR054: 73, AR051: 55, AR089: 21, AR061: 8		
							H0415: 1		
HOFMT45	891512	2312	3 - 269	4999	Asp-1 to Leu-10, Glu-38 to Cys-74.		AR051: 10, AR054: 9, AR050: 2		
							H0415: 1		
HOFMS43	947973	2313	3 - 359	5000	Asp-1 to Asp-17, Pro-61 to Asn-66, Tyr-84 to Tyr-90, Ser-103 to Trp-110.		AR051: 15, AR050: 9, AR089: 7, AR061: 5, AR054: 1		
							H0415: 1		
HOFMS09	972725	2314	3 - 461	5001			H0415: 1		

HOFMP09	943358	2315	1 - 372	5002	Ala-74 to Gly-84, Arg-98 to Lys-104.	AR089: 20, AR061: 9 H0415: 1		
HOFMI25	491360	2316	145 - 2	5003	Lys-28 to Val-33, Gln-40 to Gly-48.	H0415: 1		
	859125	2687	3 - 839	5374	Asn-33 to Leu-38.			
HOFMF82	693987	2317	2 - 169	5004	Thr-1 to Lys-7, Ala-17 to Arg-33, His-35 to Asn-45, Glu-47 to Arg-52.	AR089: 2, AR061: 1 H0415: 1		
	694062	2688	3 - 476	5375	Phe-8 to Ser-21, Ile-28 to Arg-33, Ile-40 to Gly-49, Ala-56 to Gln-61, Gln-69 to Ser-76, Ala-91 to Tyr-96, Thr-119 to Cys-126, Ser-132 to Arg-144, Thr-147 to Asp-158.			
	909248	2689	1 - 447	5376	Arg-17 to Leu-32, His-43 to Cys-54.			
HOFMF81	788733	2318	3 - 395	5005	Asp-1 to Asn-6, Met-46 to Phe-53.	H0415: 1		
HOFMF19	888780	2319	2 - 397	5006	Arg-1 to Gly-14, Glu-35 to Leu-42, Thr-54 to Lys-61.	AR050: 21, AR051: 10, AR054: 9 H0415: 1		
	942367	2320	271 - 993	5007		H0414: 1		
HOFAF25	886485	2321	3 - 527	5008	Pro-19 to Arg-27, Ser-36 to Asn-42, His-101 to Pro-107, Gly-150 to Gln-155,	AR054: 15, AR051: 3, AR050: 0 H0414: 1		

HODKG07	951875	2322	3 - 143	5009	Ser-167 to Thr-175. Gly-13 to Ser-20, Arg-41 to Thr-47.	L0623: 2, H0615: 1 and L0519: 1.		
HODJU05	929321	2323	91 - 309	5010	Arg-52 to Asn-61.	H0615: 1, L0435: 1 and L0759: 1.		
HODJL04	926200	2324	128 - 328	5011		H0615: 1, L0520: 1 and L0766: 1.		
HODHK07	952193	2325	114 - 278	5012	Thr-26 to Ser-33.	H0615: 1 and L0754: 1.		
HODHG11	966063	2326	338 - 610	5013	Arg-1 to Val-10, Trp-12 to Tyr-20, Arg-47 to Ser-63.	H0615: 1 and L0758: 1.		
HODGL88	859300	2327	461 - 610	5014	Arg-8 to Arg-16.	L0471: 1, H0615: 1, L0748: 1 and L0749: 1.		
HODGJ02	918476	2328	237 - 368	5015		L0471: 1, H0615: 1 and L0748: 1.		
HODFY10	963350	2329	122 - 358	5016	Asn-1 to Asp-6, Phe-8 to Ser-14.	L0777: 2 and H0615: 1.		
HODFX19	842138	2330	3 - 494	5017	Pro-15 to Gly-24, Cys-36 to Ile-44, Arg-77 to Pro-112.	H0615: 1 and L0775: 1.		
HODFX12	969588	2331	3 - 170	5018	Ser-17 to Gln-29.	H0615: 1 and L0666: 1.		
HODFX04	926278	2332	222 - 491	5019	Ser-2 to Ile-16.	H0615: 1, L0775: 1 and L0748: 1.		
HODFW95	795281	2333	3 - 563	5020	His-1 to Arg-7, Ala-45 to Arg-52, Ser-75 to Leu-80, Arg-89 to Asp-94,	L0747: 2 and H0615: 1.		

HODFW40	859320	2334	386 - 556	5021	Arg-139 to Glu-158.	H0615: 1, L0805: 1 and L0776: 1.		
HODFR85	783789	2335	35 - 199	5022		H0615: 1 and L0756: 1.		
HODFL37	948703	2336	239 - 463	5023	Lys-1 to Thr-22.	H0615: 1		
HODFJ11	966065	2337	326 - 460	5024		L0777: 2 and H0615: 1.		
HODFI66	974317	2338	81 - 338	5025		H0615: 1		
HODFH45	974916	2339	453 - 593	5026		H0615: 1		
HODFG82	779191	2340	1 - 150	5027		H0615: 1 and L0362: 1.		
HODFF88	974911	2341	14 - 544	5028	His-8 to Gly-18, Glu-150 to Leu-167.	AR054: 34, AR051: 29, AR050: 23, AR089: 4, AR061: 4 H0615: 1		
HODFE04	926999	2342	85 - 249	5029		H0615: 1 and L0748: 1.		
HODFD73	909812	2343	1 - 576	5030		AR061: 10, AR089: 4 H0615: 1		
HODFC79	774156	2344	66 - 242	5031	Thr-47 to Lys-53:	H0615: 1 and L0749: 1.		
HODEZ45	974337	2345	215 - 436	5032	His-34 to Trp-39.	H0615: 1		
HODEU01	915167	2346	2 - 286	5033		L0748: 3 and H0615: 1.		
HODET07	952194	2347	354 - 127	5034		H0615: 1 and L0748: 1.		
HODES10	963474	2348	90 - 200	5035		L0534: 1 and H0615: 1.		



HODEO35	859364	2349	2 - 136	5036		H0615: 1, L0376: 1 and L0759: 1.		
HODEK82	779245	2350	420 - 596	5037	Leu-1 to Phe-8.	H0615: 1 and L0753: 1.		
HODEA14	859375	2351	3 - 527	5038		H0615: 1, L0060: 1 and L0462: 1.		
HODDX64	745810	2352	73 - 393	5039		H0328: 1 and L0748: 1.		
HODDS89	531075	2353	301 - 453	5040	Thr-1 to Val-7.	H0328: 1 and L0756: 1.		
HODDS74	765863	2354	83 - 235	5041	Arg-21 to Phe-27, Ser-45 to Trp-50.	H0328: 1 and L0748: 1.		
HODDF37	420051	2355	271 - 420	5042		H0328: 1		
	704622	2690	173 - 481	5377	Pro-46 to Tyr-51.			
HODDE02	920961	2356	3 - 200	5043	Asp-1 to Asp-8.	H0328: 1, L0373: 1 and L0777: 1.		
HODCZ64	745966	2357	71 - 208	5044	Pro-35 to Lys-46.	AR051: 30, AR050: 10 H0328: 1		
HODCZ39	875811	2358	3 - 203	5045		H0328: 1, L0748: 1 and L0596: 1.		
HODCY73	764543	2359	214 - 414	5046	Asn-36 to Thr-47.	H0328: 1, L0748: 1 and L0439: 1.		
HODCY32	859543	2360	212 - 352	5047		H0328: 1		
HODCW83	781287	2361	40 - 207	5048		H0328: 1 and L0777: 1.		
HODCV61	868291	2362	187 - 393	5049		H0328: 1		
HODCO15	660502	2363	82 - 219	5050		H0328: 1 and L0748: 1.		
HODCI84	973286	2364	28 - 354	5051	Ser-51 to Leu-56,	H0328: 1		

HODCC05	932633	2365	397 - 552	5052	Ser-84 to Leu-90. Val-10 to Glu-16.	H0328: 1, L0455: 1 and L0777: 1.		
HODCA90	792611	2366	62 - 313	5053	Asn-44 to Asn-51.	H0328: 1 and L0749: 1.		
HODBZ85	784526	2367	60 - 236	5054		H0328: 1 and L0748: 1.		
HODBX08	960178	2368	344 - 595	5055	Pro-43 to Ser-54.	H0328: 1, L0527: 1 and L0749: 1.		
HODBU72	766284	2369	99 - 266	5056	Pro-33 to Phe-39, Tyr-50 to Ser-56.	L0598: 2 and H0328: 1.		
HODBK84	859558	2370	203 - 460	5057	Gly-1 to Ser-17.	AR051: 91, AR050: 61, AR054: 56 H0328: 1		
HODBF61	742114	2371	1 - 159	5058	Tyr-35 to Ile-42.	H0328: 1		
HODBF40	529387	2372	24 - 215	5059		H0328: 1		
HODBF33	702750	2373	2 - 193	5060	Leu-1 to Gly-12.	L0794: 2, L0750: 2, H0328: 1, L0766: 1, L0803: 1, L0788: 1 and L0755: 1.		
HODBF17	529389	2374	196 - 336	5061		H0328: 1 and L0792: 1.		
HODBD93	792579	2375	126 - 308	5062	His-1 to Gly-6, Cys-9 to Thr-18.	L0731: 2 and H0328: 1.		
HODBD73	764670	2376	104 - 340	5063	Thr-8 to Arg-14, Ser-37 to Glu-42.	H0328: 1 and L0748: 1.		
HODBC42	529635	2377	280 - 486	5064	Ser-8 to Ser-13.	L0731: 3 and H0328: 1.		
HODBA48	721931	2378	18 - 257	5065		L0745: 2, H0328: 1,		

HODAZ21	826693	2379	2 - 205	5066	Glu-1 to Gly-13, Gly-21 to Thr-28, Lys-43 to Asn-61.	L0740: 1 and L0759: 1. H0328: 1		
HODAX45	723449	2380	2 - 103	5067	Pro-1 to Gly-12.	L0748: 2 and H0328: 1.		
HODAV84	592179	2381	43 - 210	5068	Lys-1 to Ser-7.	H0328: 1		
HODAV24	679165	2382	177 - 308	5069		L0748: 3, L0740: 2, H0328: 1, L0766: 1, L0803: 1, L0659: 1, L0665: 1 and L0612: 1.		
HODAK55	745532	2383	2 - 169	5070		AR061: 11, AR089: 9 L0748: 3 and H0328: 1.	230400, 250250	
HODAK05	932639	2384	2 - 133	5071	Arg-15 to Thr-22, Ser-28 to Arg-33.	H0328: 1 and L0596: 1.		
HODAE72	529638	2385	1 - 135	5072		H0328: 1		
HODAE55	529637	2386	1 - 117	5073		H0328: 1		
HODAE48	529639	2387	21 - 101	5074	Asp-1 to Arg-8.	H0328: 1		
HODAE01	921680	2388	92 - 319	5075		H0328: 1 and L0748: 1.		
HODAA92	790588	2389	77 - 253	5076	Pro-1 to Gly-20, Ser-27 to Ser-34.	H0328: 1		
HODAA85	784534	2390	3 - 167	5077		H0328: 1		
HODAA80	529560	2391	2 - 298	5078		H0328: 1		
HODAA69	529563	2392	113 - 238	5079		H0328: 1		
HODAA54	859582	2393	64 - 198	5080	Tyr-15 to Gln-27.	H0328: 1		
HODAA34	529570	2394	93 - 251	5081	Lys-42 to Thr-47.	H0328: 1		
HODAA21	859583	2395	49 - 198	5082		H0328: 1 and L0605:		

HODAA15	523382	2396	84 - 131	5083			1.	
HODAA07	954157	2397	21 - 107	5084			H0328: 1	
HODAA04	927711	2398	58 - 303	5085			H0328: 1	
HOCPU05	928651	2399	114 - 377	5086			L0755: 2, L0758: 2, L0717: 1, L0365: 1 and H0660: 1.	
HOCPH02	917453	2400	139 - 327	5087		Arg-14 to Cys-20, Val-34 to Cys-43, Pro-45 to Ser-52.	L0748: 2, L0756: 2, L0372: 1, L0663: 1, L0665: 1, H0660: 1, L0439: 1 and L0777: 1.	
HOCPF02	917630	2401	49 - 240	5088		Ser-18 to Ser-27.	L0766: 1, H0660: 1 and L0758: 1.	
HOCOV07	951744	2402	108 - 314	5089		Phe-19 to Tyr-34, Ser-41 to Arg-51.	L0766: 3 and H0660: 1.	
HOCMM01	914464	2403	112 - 390	5090		Ser-19 to Tyr-28, Glu-34 to Val-45, Gly-53 to Pro-58, Glu-63 to Gln-82.	L0763: 1, L0776: 1 and H0660: 1.	
HOCMI24	878363	2404	2 - 484	5091		Asp-21 to Leu-45.	H0660: 1 and L0731: 1.	
HOCMC01	914552	2405	432 - 136	5092		Pro-31 to Gly-36, Ser-60 to Leu-65, Gln-69 to Thr-76, Gly-81 to Glu-87.	H0660: 1 and L0749: 1.	
HNOIJ12	969077	2406	1517 - 1771	5093			H0687: 1, L0803: 1 and L0666: 1.	
HNOAD04	926258	2407	464 - 625	5094		Thr-12 to Ser-19, Lys-28 to Ala-39.	L0766: 4, L0439: 4, L0646: 1, H0651: 1.	

HNNNB08	957719	2408	358 - 161	5095			L0756: 1 and L0759: 1.		
HNNNA07	899742	2409	588 - 361	5096			H0678: 1		
							AR051: 4, AR054: 0		
							H0678: 1		
HNIAB92	683077	2410	111 - 1	5097		Gln-27 to Asn-35.	S0326: 1		
HNIAB73	764172	2411	2 - 346	5098			S0326: 1		
HNIAB26	974750	2412	387 - 73	5099		Arg-14 to Trp-19.	S0326: 1, L0769: 1 and L0774: 1.		
HNBVH02	917719	2413	91 - 192	5100			H0662: 1 and L0748: 1.		
HNBVC03	922402	2414	3 - 104	5101		Tyr-6 to Thr-15.	H0662: 1 and L0766: 1.		
HNBUC06	933673	2415	321 - 521	5102		Glu-1 to Tyr-7, Pro-42 to Leu-47, Pro-50 to Ala-57.	H0662: 1, L0794: 1 and L0758: 1.		
HNBUC01	914361	2416	109 - 336	5103		His-1 to Phe-6, Asn-58 to Met-65.	H0662: 1 and L0524: 1.		
HNBUI10	961734	2417	3 - 437	5104		Pro-6 to Cys-24, Glu-26 to Trp-37, Asn-65 to Leu-73, Gln-81 to Gly-90, Gly-100 to Gly-115, Asn-118 to Ser-126.	H0662: 1, L0764: 1, L0803: 1, L0774: 1, L0758: 1 and L0599: 1.		
HLWFI69	754476	2418	3 - 245	5105			H0553: 1 and L0754: 1.	12q13.3	181430, 232800, 600808, 601284, 601769, 601769, 602116

HLWFB01	915399	2419	56 - 328	5106	Lys-38 to Gly-43.	H0553: 1 and L0794: 1.		
HLWEH10	963548	2420	1 - 204	5107	Gln-1 to Ala-17, Arg-47 to Gln-52.	L0617: 1 and H0553: 1.		
HLWEA90	787632	2421	179 - 331	5108	Lys-1 to Thr-6, Ser-32 to Ser-38.	H0553: 1 and L0747: 1.		
HLWDZ31	917643	2422	2 - 259	5109		H0553: 1 and L0758: 1.	20q13.1	256540, 600281, 600281
HLWDD01	915378	2423	1 - 216	5110	Trp-5 to Lys-11.	H0553: 1 and L0512: 1.		
HLWDB48	856512	2424	215 - 514	5111	Pro-31 to Gln-38, Ser-58 to Gly-69.	H0553: 1 and L0740: 1.		
HLWCP60	739801	2425	1 - 207	5112	Phe-1 to Gly-6, Phe-40 to Gly-49.	H0553: 1 and L0596: 1.		
HLWCN93	791854	2426	219 - 392	5113	Glu-4 to Ala-9.	H0553: 1 and L0748: 1.		
HLWCN50	723787	2427	2 - 250	5114	Val-33 to Ser-38.	H0553: 1 and L0756: 1.		
HLWCF83	781069	2428	1 - 297	5115	Pro-14 to Arg-26, Pro-28 to Ser-33, Gly-48 to Ala-56.	H0553: 1 and L0752: 1.		
HLWCF33	687995	2429	3 - 503	5116	Leu-62 to Arg-69, Lys-76 to Phe-96.	H0553: 1, L0591: 1 and L0595: 1.		
HLWCE47	720156	2430	278 - 466	5117		H0553: 1, L0783: 1 and L0749: 1.		
HLWCB93	623773	2431	278 - 3	5118	Pro-6 to Glu-18, Pro-20 to Trp-40, Lys-86 to Arg-92.	H0553: 1		

HLWBX42	856519	2691	3 - 200	5378	Ser-15 to Ser-23.				
	917920	2432	44 - 382	5119	Arg-11 to Ser-17.			H0553: 1 and L0751: 1.	
HLWBW29	690515	2433	1 - 195	5120	Arg-2 to Gly-7, Ile-28 to Ile-34, Ser-56 to Val-62.			H0553: 1 and L0748: 1.	
HLWBT09	887877	2434	3 - 419	5121	Ser-1 to Glu-28.			AR050: 49, AR054: 47, AR051: 27 H0553: 1	
HLWBS62	743406	2435	9 - 365	5122	Gly-11 to Trp-16, Cys-53 to Gly-78, Arg-99 to Asp-105, Ser-113 to Glu-119.			H0553: 1, L0766: 1 and L0747: 1.	
HLWBR85	784261	2436	221 - 370	5123	Lys-9 to Asn-22.			L0747: 2 and H0553: 1.	
HLWBQ91	790072	2437	1 - 303	5124				H0553: 1 and L0748: 1.	136550, 602772
HLWBJ65	747784	2438	270 - 467	5125	Leu-20 to Asp-38.			H0553: 1 and L0759: 1.	
HLWBH92	791355	2439	95 - 301	5126	Glu-8 to Gln-18.			H0553: 1 and L0754: 1.	
HLWBG78	888068	2440	39 - 371	5127	Pro-2 to Thr-7, Ala-13 to Arg-20.			H0553: 1 and L0748: 1.	
HLWBF48	721530	2441	172 - 381	5128	Arg-12 to Gly-21.			H0553: 1, L0665: 1, L0439: 1 and L0759: 1.	
HLWBE74	887967	2442	2 - 232	5129	Glu-7 to Glu-13, Trp-18 to Thr-32, Pro-34 to Arg-44, Gly-51 to Trp-60, Pro-62 to Ala-72.			AR054: 15, AR050: 3, AR051: 2 H0553: 1	

HLWBC21	869611	2443	2 - 412	5130	Pro-2 to Val-21, Asp-23 to Val-30, Gly-36 to Leu-41, Met-49 to Gly-55, Thr-72 to Lys-78, Ile-92 to Asp-97.	L0747: 2, H0553: 1 and L0794: 1.		
HLWBA80	720397	2444	3 - 347	5131	Lys-6 to Leu-12, His-39 to Leu-57, Ile-61 to Asp-66.	H0553: 1 and L0755: 1.		
HLWBA27	931387	2445	2 - 322	5132	Lys-6 to Asn-13, Gly-31 to Gly-36, Glu-91 to Ser-99.	H0553: 1 and L0749: 1.		
HLWAW86	785395	2446	1 - 273	5133	Lys-11 to Arg-23, Cys-25 to Cys-31, Pro-33 to Tyr-38, Arg-46 to Ile-60.	H0553: 1 and L0759: 1.		
	941397	2692	115 - 462	5379	Leu-17 to Gln-23, Gln-38 to Phe-44, Gln-65 to Gln-72, Thr-80 to Tyr-86.			
HLWAS09	625419	2447	74 - 235	5134	His-27 to Ile-34.	H0553: 1		
HLWAR08	959139	2448	3 - 290	5135	Tyr-46 to His-52.	AR089: 4, AR061: 2 L0539: 1 and H0553: 1.		
HLWAO67	751503	2449	35 - 214	5136		H0553: 1 and L0745: 1.		
HLWAL31	948928	2450	124 - 2	5137		AR054: 55, AR050: 51, AR051: 48, AR089: 4, AR061: 2 H0553: 1		



	971312	2693	23 - 511	5380	Arg-9 to Pro-15, Leu-114 to Val-120, Cys-147 to Cys-156.				
HLWAJ18	666281	2451	41 - 214	5138		H0553: 1 and L0439: 1.	20q12-q13	600281, 600281	
HLWAF02	919714	2452	156 - 449	5139	Arg-1 to Ser-6, Phe-13 to Gln-24, Glu-31 to Arg-40, Ser-48 to Asn-56, Asp-69 to Val-75.	H0553: 1 and L0758: 1.			
HLWAE09	789030	2453	444 - 133	5140	Pro-21 to Gln-27, Glu-53 to Ser-60.	H0553: 1 and L0439: 1.			
HLWAD57	734655	2454	2 - 166	5141	His-1 to Ala-7, Thr-34 to Leu-39.	H0553: 1			
HLWAD33	702317	2455	190 - 468	5142	Arg-1 to Arg-10, Ile-66 to Glu-78.	H0553: 1, L0754: 1 and L0755: 1.			
HLWAD32	699158	2456	49 - 219	5143	Asn-42 to Lys-48.	H0553: 1			
HLWAD02	919725	2457	13 - 252	5144	Arg-2 to Phe-7, Thr-68 to Asn-73.	H0553: 1 and L0663: 1.			
HKZAH11	965175	2458	1 - 324	5145	Gly-11 to Ile-17, Asn-24 to Ser-31, Gln-47 to Ala-64, Pro-66 to Ala-72, Gly-77 to Gly-84.	L0794: 2, L0766: 1, L0665: 1 and H0689: 1.			
HJMBX19	668568	2459	2 - 286	5146	Leu-2 to Arg-11, Ser-25 to Gly-33, Lys-54 to His-64.	L0777: 2, H0545: 1 and L0754: 1.			
HJMB577	772101	2460	158 - 328	5147	Ser-48 to Lys-57.	H0545: 1 and L0756: 1.			
HJMB510	964464	2461	96 - 380	5148	Tyr-47 to Ser-58.	H0545: 1 and L0599:			

HJMBQ90	788834	2462	156 - 557	5149	Thr-17 to Gly-22, Gln-69 to Glu-74.	1. H0545: 1 and L0747: 1.		
HJMBN02	919737	2463	218 - 436	5150	Arg-5 to Thr-16.	H0545: 1 and L0763: 1.		
HJMBI93	929114	2464	47 - 199	5151		H0545: 1 and L0646: 1.		
HJMAV93	828110	2465	373 - 122	5152	Asn-74 to Pro-80.	H0545: 1, L0748: 1 and L0740: 1.		
HJMAU07	961623	2466	187 - 501	5153		H0545: 1 and L0794: 1.	16p13.3	141750, 141800, 141800, 141800, 141800, 141850, 141850, 141850, 141850, 141850, 141850, 141850, 156850, 186580, 191092, 600140, 600273, 601313, 601785
HJMAQ86	785410	2467	1 - 234	5154	Pro-3 to Ser-16, Pro-27 to Gly-32, Pro-49 to Ala-58, Thr-70 to Lys-78.	L0588: 2, H0545: 1 and L0603: 1.		

HJMAQ14	657579	2468	130 - 477	5155			L0163: 2, H0545: 1 and L0754: 1.		
HJMAJ91	811222	2469	78 - 452	5156	Arg-1 to Ser-15, Ser-18 to Ser-33, Glu-42 to Arg-51.		H0545: 1 and L0740: 1.		
HJMAI62	742612	2470	195 - 356	5157	Gly-15 to Glu-21.		H0545: 1		
HETLF29	909762	2471	3 - 416	5158			AR061: 4, AR089: 2 H0046: 1 and L0758: 1.		
HETJY68	752542	2472	109 - 306	5159			H0046: 1, L0439: 1, L0740: 1 and L0591: 1.		
HETID12	655199	2473	13 - 321	5160	Pro-39 to Arg-44, Ala-89 to Glu-103.		H0046: 1 and L0731: 1.		
HETHO01	921649	2474	218 - 415	5161			L0748: 2, H0046: 1 and L0766: 1.		
HETHB18	529467	2475	2 - 247	5162			H0046: 1		
HETFF68	529587	2476	2 - 166	5163	Asn-1 to Leu-13.		H0046: 1		
HETFF43	529589	2477	70 - 204	5164			H0046: 1		
HETDU61	742157	2478	250 - 420	5165	Ala-39 to Cys-46.		H0046: 1, L0748: 1 and L0581: 1.		
HETDA25	677490	2479	181 - 336	5166			H0046: 1 and L0439: 1.		
HETCO27	533536	2480	3 - 113	5167	Val-19 to Leu-35.		H0046: 1		
HETCH01	961038	2481	2 - 352	5168	Cys-11 to Pro-19, Asn-28 to Leu-35.		L0738: 1, H0046: 1, L0527: 1 and L0599: 1.		
HETBM55	929285	2482	113 - 343	5169	Val-20 to Gly-26, Asn-62 to Arg-68.		L0747: 2 and H0046: 1.	1q12-1q21.2	104770, 107670, 110700, 145001,

									146760, 146790, 159001, 191315, 600897, 601412, 601652, 601863, 602491
HETBE61	965638	2483	124 - 447	5170	Glu-31 to Gly-37, Leu-42 to Gln-49.	H0046: 1 and L0731: 1.	6q25		180020, 600320, 600883
HETAS91	790499	2484	237 - 548	5171	Ser-73 to Lys-91.	L0740: 3 and H0046: 1.			
HETAS81	778539	2485	12 - 188	5172	Pro-17 to Ser-23.	H0046: 1 and L0777: 1.			
HETAS62	754155	2486	14 - 187	5173	Ser-22 to Lys-31, Thr-39 to Glu-47.	H0046: 1 and L0748: 1.			
HETAJ14	660831	2487	575 - 757	5174	Ala-24 to Ser-31, Val-52 to Asp-61.	L0747: 2, H0046: 1 and L0748: 1.			
HEQCC01	924849	2488	375 - 659	5175	Ser-54 to Ala-59, Ser-64 to Phe-69, Arg-79 to Thr-87.	H0544: 1, L0775: 1, L0776: 1 and L0758: 1.			
HEQBT78	773528	2489	252 - 10	5176		H0544: 1 and L0731: 1.			
HEQBPI8	855578	2490	463 - 245	5177	Thr-7 to Gly-14.	H0544: 1			
HEQBI09	739877	2491	29 - 142	5178		H0544: 1			
HEQBG85	827915	2492	1 - 276	5179		H0544: 1	2pter-p25.1		
HEQBG60	427813	2493	2 - 295	5180	Ser-1 to Pro-23, Pro-35 to Asn-45,	H0544: 1	17p13.3	113721, 247200,	

HEQBE78	772860	2494	101 - 265	5181	Cys-53 to Arg-70.			600059, 601545
HEQBE71	760305	2495	101 - 451	5182	Asp-13 to Lys-20, Thr-43 to Ala-49.	H0544: 1		
HEQAZ01	916321	2496	97 - 402	5183	Glu-18 to Pro-27, Asp-58 to Asn-65.	H0544: 1		
HEQAM59	739220	2497	50 - 160	5184	Phe-2 to Gly-7.	H0544: 1 and L0599: 1.		
HEQAK94	793250	2498	2 - 298	5185		H0544: 1 and L0752: 1.		
HEQAF54	729594	2499	3 - 200	5186		H0544: 1, L0439: 1 and L0754: 1.		
HEQAD73	914044	2500	82 - 555	5187	Trp-1 to Ser-10.	L0439: 2 and H0544: 1.		
HEQAA93	792255	2501	340 - 519	5188	Lys-6 to Arg-11, Thr-22 to Gly-34.	L0731: 5 and H0544: 1.		
HEPCB04	941270	2502	72 - 305	5189	Ser-1 to Gln-9, Ser-16 to Cys-22, Ser-33 to Ser-38, Ser-58 to Trp-66.	L0747: 3 and H0544: 1.		
HEPBO92	952996	2503	146 - 349	5190	Arg-10 to Ser-18, Leu-37 to Arg-48.	L0777: 4, H0150: 1 and L0757: 1.		
HEPBO85	783362	2504	1 - 240	5191		H0150: 1 and L0747: 1.		
HEPAY26	825778	2505	29 - 193	5192		L0754: 2 and H0150: 1.		
HEPAX40	535627	2506	2 - 172	5193		H0150: 1 and L0743: 1.		
						L0744: 2, L0731: 2 and		

HEPAX16	667665	2507	1 - 330	5194	H0150: 1, L0766: 3, L0776: 2, H0150: 1, L0371: 1, L0761: 1, L0764: 1, L0662: 1, L0655: 1, L0748: 1, L0754: 1, L0749: 1 and L0779: 1.	11p15.5	125852, 126452, 126452, 141900, 141900, 141900, 141900, 141900, 141900, 141900, 141900, 142000, 142000, 142200, 142250, 142270, 176730, 176730, 176730, 190020, 191290, 192500, 192500, 194071, 194071, 204500, 600856, 601680, 602631, 602631
HEPAQ35	707533	2508	245 - 511	5195	L0748: 2, L0756: 2,		

								L0777: 2, H0150: 1, L0789: 1, L0666: 1 and L0758: 1.			
HEPAP34	703336	2509	369 - 623	5196			Pro-17 to Val-26, His-34 to Lys-41, Pro-54 to Phe-66.	H0150: 1 and L0777: 1.			
HEPAN05	932893	2510	223 - 489	5197			Lys-15 to Leu-29, Lys-45 to Glu-55, Lys-82 to Lys-89.	H0150: 1 and L0780: 1.			
HEPAK04	933039	2511	4 - 177	5198			Leu-42 to Gly-54.	H0150: 1 and L0763: 1.			
HEPAJ14	657440	2512	55 - 243	5199			His-1 to Ser-10, Pro-22 to Gly-38, Asn-55 to Ser-60.	H0150: 1 and L0743: 1.			
HEPAJ04	933091	2513	71 - 367	5200			Thr-1 to Arg-16, Ala-45 to Gln-50, Pro-63 to Ala-68, Ala-80 to Asp-93.	H0150: 1, L0779: 1 and L0758: 1.			
HEPAE58	509130	2514	174 - 353	5201			Gly-38 to Asp-56.	H0150: 1 and L0743: 1.			
HEPAE02	921389	2515	3 - 107	5202			Leu-15 to Lys-24.	H0150: 1 and L0522: 1.			
HEGBC03	922550	2516	2 - 304	5203				H0550: 1 and L0646: 1.			
HEGBB67	751233	2517	95 - 352	5204			Val-6 to Glu-11, Phe-22 to Cys-29.	H0550: 1 and L0745: 1.			
HEGBA01	915596	2518	217 - 372	5205				H0550: 1 and L0605: 1.			
HEGAX04	927260	2519	3 - 230	5206			Lys-18 to Glu-23, Gln-60 to Ala-67.	H0550: 1 and L0766: 1.			

HEGAQ91	789940	2520	1 - 273	5207			H0550: 1, L0748: 1 and L0749: 1.	Xq22.3	300067, 300067, 300121, 300121, 301201, 301835, 311850
HEGAL55	731654	2521	153 - 359	5208	Lys-5 to Gly-11.		H0550: 1, L0745: 1 and L0731: 1.		
HEGAJ08	959216	2522	344 - 511	5209	Pro-7 to Val-13.		L0731: 2, L0597: 2, H0550: 1, L0783: 1 and L0439: 1.		
HEGAC02	918992	2523	2 - 196	5210	Ser-7 to Cys-21, Ile-59 to Gly-64.		H0550: 1 and L0758: 1.		
HEEAY84	782706	2524	222 - 383	5211	Asn-1 to Lys-14.		H0549: 1 and L0748: 1.		
HEEAX09	912065	2525	2 - 328	5212	Arg-65 to Arg-72.		AR051: 4, AR050: 2, AR054: 2 H0549: 1		
HEEAW40	710655	2526	222 - 398	5213	Asn-45 to Thr-50, Pro-52 to Arg-57.		H0549: 1, L0589: 1 and L0366: 1.	6q25.2-q27	152200, 167000, 180020, 600320, 600883, 602544
HEEAP59	738892	2527	249 - 413	5214	Leu-32 to Leu-38.		H0549: 1 and L0594: 1.		
HEEAM25	677599	2528	101 - 784	5215			L0794: 6, L0806: 2, L0752: 2, H0549: 1, L0796: 1, L0766: 1,		



								L0380: 1, L0803: 1, L0804: 1, L0807: 1, L0789: 1, L0663: 1, L0755: 1, L0596: 1 and L0485: 1.			
HEEAH94	794257	2529	114 - 344	5216				H0549: 1 and L0599: 1.			
HEEAH76	769950	2530	16 - 213	5217			Val-21 to Gly-26, Leu-29 to Gly-38.	H0549: 1 and L0748: 1.			
HEEAH57	734488	2531	219 - 404	5218			Pro-3 to Phe-9, Ser-17 to Ala-24, Val-52 to Lys-62.	H0549: 1 and L0601: 1.			
HEEAH16	661827	2532	15 - 344	5219			Ser-45 to Ser-50, Tyr-103 to Phe-110.	H0549: 1 and L0747: 1.			
HEEAG51	930810	2533	1 - 423	5220			Glu-61 to Val-77, Phe-81 to Ser-88.	H0549: 1 and L0605: 1.			
HEEAG12	724929	2534	266 - 36	5221			Thr-29 to Pro-49, Asp-65 to Glu-77.	AR050: 66, AR054: 64, AR051: 63, AR089: 13, AR061: 3 H0549: 1			
	887048	2694	429 - 295	5381							
HEEAD13	470886	2535	1 - 195	5222				H0549: 1 and L0756: 1.			
HEEAB40	710668	2536	128 - 310	5223			Val-15 to Ala-23, Pro-30 to Ser-35.	H0549: 1 and L0748: 1.			
HEAAX26	684734	2537	63 - 182	5224			Val-22 to Gly-29.	H0369: 1 and L0740: 1.			
HEAAU20	911255	2538	53 - 364	5225			Lys-80 to Lys-86.	H0369: 1 and L0745: 1.	6q21	120110, 121014, 601666,	

HEAAR47	973284	2539	20 - 220	5226				602772
HEAAR21	883939	2540	353 - 535	5227	Gly-1 to Ser-6.	H0369: 1		
HEAAN43	842032	2541	235 - 336	5228		H0369: 1 and L0769: 1.		
HEAAM71	950736	2542	321 - 563	5229	Thr-3 to Ala-10, Glu-30 to Arg-38.	H0369: 1 and L0748: 1.		
HEAAL76	770200	2543	2 - 136	5230	Leu-23 to His-28.	H0369: 1 and L0589: 1.		
HEAAG84	896892	2544	605 - 396	5231		H0369: 1		
	904209	2695	1539 - 1913	5382	Arg-43 to Ser-49, Glu-55 to Ser-61, Pro-70 to Arg-75, Cys-91 to Gly-103.			
	906483	2696	316 - 504	5383	Arg-45 to Gly-52.			
HEAAG42	714041	2545	598 - 792	5232	Glu-24 to Tyr-31.	L0731: 9, L0754: 3 and H0369: 1.		
HEAAB66	844361	2546	438 - 740	5233		H0369: 1		
HCORB05	928679	2547	2 - 142	5234	Pro-1 to Arg-14.	L0626: 1, L0775: 1, L0776: 1 and H0670: 1.		
HCOPM06	933473	2548	158 - 628	5235	Pro-15 to Glu-21, Ala-43 to Glu-58, Leu-96 to Glu-101, Ala-111 to Ala-119.	L0769: 1, L0665: 1 and H0670: 1.		
HCOP107	951645	2549	185 - 313	5236	Thr-29 to Arg-43.	H0670: 1 and L0758: 1.		
HCOPF07	951655	2550	79 - 240	5237		L0779: 3, L0758: 3 and H0670: 1.		

HCOOF07	951693	2551	221 - 493	5238	Pro-13 to Ser-19, Asp-27 to Thr-35. Asn-7 to Val-13.	H0670: 1, L0731: 1 and L0759: 1.		
HCONP02	917577	2552	148 - 306	5239	Asp-5 to Ala-11, Trp-24 to Phe-31, Arg-44 to Trp-50.	L0517: 1, L0438: 1, H0670: 1 and L0439: 1.		
HCONM33	971637	2553	474 - 217	5240	Gln-19 to Asp-38, Pro-46 to Thr-55, Leu-96 to Gly-104, Ala-114 to Ala-119, Gln-125 to Trp-131, Pro-133 to Pro-141, Phe-144 to Glu-150, Glu-180 to Val-185, Glu-192 to Glu-197, Glu-254 to Leu-262, Met-272 to Ser-280.	L0517: 2, L0756: 2, L0803: 1, L0776: 1, L0809: 1, L0663: 1, H0670: 1, L0755: 1 and L0759: 1.		
HCOMM05	925952	2554	1 - 840	5241	Cys-6 to Lys-21, Ser-53 to Ile-65, Asn-68 to Gln-80, Arg-106 to Ala-114.	AR089: 1, AR061: 1 H0670: 1		
HCHQA48	908495	2555	13 - 357	5242	Arg-1 to Lys-12, Gly-57 to Gly-62, Pro-74 to Asp-80.	H0484: 1 and L0743: 1.		
HCHOX63	957690	2556	1 - 741	5243	Lys-1 to Ser-13.	H0484: 1, L0617: 1, L0772: 1, L0751: 1 and L0752: 1.		
HCHNW48	862478	2557	122 - 325	5244		AR061: 1, AR089: 1 H0484: 1 and L0589: 1.		

HCHMX82	850340	2558	2 - 349	5245			H0484: 1 and L0749: 1.		
HCHMW18	966985	2559	97 - 408	5246		Leu-8 to Val-20, Arg-25 to Arg-35, Ala-38 to Trp-46, Phe-69 to Tyr-75, Ser-96 to Trp-104.	L0757: 2 and H0484: 1.		
HCHMJ89	786765	2560	3 - 218	5247		Ala-1 to Gly-8, Arg-16 to Ser-21, Ser-35 to Pro-45, Ala-61 to Gly-67.	H0484: 1 and L0439: 1.		
HCHMP96	800129	2561	3 - 248	5248			AR051: 32, AR054: 29, AR050: 28 H0484: 1		
HCHMP15	935298	2562	52 - 591	5249		Lys-67 to Ser-79, Ser-89 to Thr-109, Asn-116 to Ser-129, Glu-140 to Lys-147, Ser-161 to Lys-172.	H0484: 1 and L0792: 1.		
HCHCI07	952957	2563	248 - 499	5250		Gly-1 to Trp-6, Gly-74 to Trp-80.	L0749: 3 and H0483: 1.		
HCHCH68	869084	2564	251 - 502	5251			H0483: 1 and L0764: 1.		
HCHCG28	686431	2565	214 - 462	5252		Phe-32 to Ala-37.	L0748: 3, L0596: 2, H0483: 1, L0439: 1 and L0749: 1.		
HCHCE78	773428	2566	11 - 193	5253			H0483: 1		
HCHBQ27	682308	2567	11 - 241	5254		Gly-4 to Lys-10, Gln-36 to Glu-41, Arg-61 to Arg-76.	H0483: 1		

HCHBN09	625420	2568	1 - 177	5255	Gly-1 to Ser-13.	H0483: 1	19q13.2	107741, 113900, 122720, 122720, 126340, 126391, 160900, 164731, 173850, 207750, 248600, 258501
HCHBM26	681404	2569	13 - 153	5256	Gly-4 to Lys-10, Gln-36 to Glu-41.	H0483: 1		
HCHAI62	743411	2570	2 - 148	5257	Lys-1 to Lys-21..	H0483: 1		
HCHAH04	487985	2571	1 - 75	5258		H0483: 1		
HCHAG52	726081	2572	3 - 212	5259	Ser-26 to Thr-44.	H0483: 1		
HCDMF96	796196	2573	86 - 286	5260	Gly-12 to Cys-27.	L0752: 1 and S0398: 1.		
HCDME32	863374	2574	147 - 473	5261	Glu-8 to Met-22, Pro-104 to Pro-109.	L0777: 1, L0758: 1, L0697: 1 and S0398: 1.		
HCDMC86	785134	2575	160 - 330	5262	Glu-12 to Leu-20.	S0398: 1		
HCDMC25	677627	2576	47 - 283	5263	Gln-9 to Val-17, Phe-38 to Glu-45.	L0439: 1 and S0398: 1.		
HCDMC23	675490	2577	116 - 271	5264		S0398: 1		
HCDMC22	672815	2578	2 - 241	5265		S0398: 1		
HCDMC06	934663	2579	28 - 183	5266		S0398: 1		
HCDMB91	789551	2580	185 - 289	5267		S0398: 1		
HCDMB42	713300	2581	128 - 244	5268	Gly-12 to His-19.	S0398: 1		
HCDMB41	711996	2582	2 - 202	5269	Gly-13 to Asn-22.	L0587: 1 and S0398: 1.		

HCDMB27	682389	2583	23 - 148	5270			S0398: 1		
HCDMB12	968918	2584	418 - 627	5271	Pro-7 to Gly-24.		AR050: 93, AR054: 62, AR051: 57 S0398: 1		
HCDMB08	958542	2585	115 - 267	5272	Gly-38 to Gly-51.		L0753: 1 and S0398: 1.		
HCDMB03	923316	2586	88 - 252	5273	Cys-20 to His-27, Glu-35 to Lys-54.		S0398: 1		
HCDMA20	669201	2587	3 - 92	5274			L0438: 1, L0439: 1 and S0398: 1.		
HCBND03	922388	2588	3 - 401	5275	Pro-12 to Thr-21, Gly-35 to Thr-41, Thr-53 to Gln-75, Ser-92 to Gly-98.		H0661: 1, L0805: 1 and L0776: 1.		
HCBMZ07	951788	2589	230 - 358	5276			H0661: 1 and L0740: 1.		
HCBMY10	961718	2590	371 - 138	5277	Glu-22 to Glu-49.		H0661: 1 and L0603: 1.		
HCBMG11	965394	2591	207 - 653	5278	Ala-1 to Asn-9, Thr-24 to Asn-29, Gly-43 to Arg-53, Arg-106 to Arg-111.		H0661: 1, L0664: 1, L0754: 1 and L0749: 1.		
HBZSK04	926407	2592	2 - 79	5279	Gln-7 to Lys-14.		S0190: 1		
HBZSG02	920249	2593	40 - 291	5280			L0771: 2 and S0190: 1.		
HBZSD32	699335	2594	59 - 427	5281	Val-8 to Leu-14, Pro-22 to Arg-31, Thr-62 to Lys-68, Arg-76 to Cys-82, Trp-85 to His-91.		S0190: 1		
HBZAJ73	764479	2595	2 - 244	5282			L0741: 3 and S0188: 1.		

HBZAJ26	681879	2596	198 - 443	5283	Gly-38 to Ser-44.	S0188: 1 and L0747: 1.		
HBZAI39	847621	2597	545 - 808	5284		S0188: 1 and L0605: 1.		
HBZAI14	847620	2598	3 - 203	5285		S0188: 1		
HBZAB15	660348	2599	240 - 362	5286	Lys-26 to His-31.	S0188: 1 and L0587: 1.		
HBZAB08	959560	2600	160 - 414	5287	Pro-1 to Gln-15, Gln-38 to Asn-45, Pro-57 to Thr-65.	L0774: 3, L0775: 1, L0809: 1, S0188: 1 and L0758: 1.		
HBNBQ50	887096	2601	222 - 473	5288	Arg-54 to Arg-60.	H0188: 1 and L0751: 1.		
HBNBO30	430360	2602	3 - 155	5289	Glu-17 to Tyr-22.	L0774: 2, L0741: 2, L0439: 2, L0411: 1 and H0188: 1.		
HBNBL29	703113	2603	245 - 409	5290		H0188: 1, L0663: 1 and L0748: 1.		
HBNBI29	907015	2604	63 - 215	5291	Trp-18 to Gly-23, Ser-25 to Met-31.	H0188: 1 and L0526: 1.		
HBNBI06	960664	2605	2 - 298	5292		H0188: 1, L0769: 1 and L0753: 1.		
HBNBB41	712676	2606	50 - 256	5293		H0188: 1 and L0748: 1.		
HBNBB27	600905	2607	143 - 3	5294		H0188: 1		
	847732	2697	1 - 186	5384				
HBNBB09	868924	2608	372 - 79	5295		L0439: 3 and H0188: 1.		
HBNAW73	764716	2609	87 - 236	5296		H0188: 1 and L0748: 1.		
HBNAC74	586797	2610	3 - 152	5297	Asp-30 to Trp-36, Ser-39 to Trp-44.	H0188: 1		
HBNAC71	525831	2611	1 - 318	5298	Arg-10 to Glu-32.	H0188: 1		

HBNAC48	721983	2612	150 - 308	5299			H0188: 1		
HBNAC42	714263	2613	1 - 120	5300			H0188: 1 and L0591: 1.		
HBNAC32	526549	2614	1 - 111	5301			H0188: 1		
HBNAC28	525832	2615	34 - 183	5302			H0188: 1		
HBNAC25	525834	2616	3 - 146	5303		Leu-2 to Gln-11, Lys-35 to Lys-48.	H0188: 1		
HBNAC09	525833	2617	8 - 76	5304			H0188: 1		
HBNAC02	921187	2618	2 - 199	5305		Pro-24 to Ala-37.	H0188: 1		
HBGTT76	903653	2619	14 - 556	5306		His-8 to Gly-18, Pro-89 to Gly-96, Lys-126 to Trp-131, Glu-133 to Gly-141.	AR050: 173, AR051: 169, AR054: 143, AR089: 46, AR061: 9 H0617: 1		
HBGTE11	965121	2620	71 - 325	5307		Gly-14 to Val-21.	H0617: 1, L0766: 1 and L0788: 1.		
HBGQS88	886650	2621	2 - 448	5308		Pro-16 to Gly-38, Arg-50 to Arg-58, Asp-65 to Asn-81.	AR054: 7, AR051: 2, AR050: 1 H0617: 1, L0769: 1, L0637: 1 and L0789: 1.		
HBGNL85	848179	2622	1 - 570	5309		Thr-10 to Gly-16.	H0617: 1, L0767: 1, L0775: 1 and L0779: 1.		
HBGND04	926973	2623	55 - 354	5310		Ser-73 to Lys-78, Pro-93 to Gly-100.	L0779: 2, L0752: 2, H0617: 1 and L0794: 1.		
HBGMT82	954374	2624	28 - 507	5311			H0617: 1, L0774: 1, L0747: 1 and L0752: 1.		
HBGMS69	754392	2625	3 - 272	5312		Pro-46 to Gly-55, Arg-79 to Cys-89.	H0617: 1 and L0750: 1.		
HBGMO78	773043	2626	104 - 307	5313		Ser-28 to Trp-36.	L0758: 2 and H0617: 1.		



HBGMG81	880276	2627	37 - 363	5314	Lys-3 to Leu-13, Pro-70 to Ser-78.	AR050: 297, AR051: 237, AR054: 211 H0617: 1		
HBGFS88	914032	2628	358 - 140	5315		L0748: 2, H0606: 1 and L0593: 1.		
HBGFG53	727748	2629	267 - 473	5316	Gly-18 to Gly-24, Gly-31 to Ser-38, His-57 to Asn-62.	H0606: 1 and L0777: 1.		
HBGDH33	702854	2630	3 - 374	5317		L0439: 6, L0776: 2, L0777: 2, H0181: 1, L0762: 1 and L0809: 1.		
HBGDF39	861602	2631	2 - 355	5318	Leu-92 to Phe-98.	AR089: 0, AR061: 0 H0181: 1		
HBGDA74	832888	2632	2 - 277	5319		AR089: 33, AR061: 29 H0181: 1	102200, 106100, 131100, 131100, 131100, 131100, 133780, 147050, 153700, 161015, 164009, 168461, 168461, 168461, 180721, 180840, 191181, 193235,	

										209901, 232600, 259700, 259770, 600045, 600319, 600528, 601884
HGBBG69	802090	2633	1 - 57	5320	Lys-8 to Ala-14.	H0181: 1				
HGBBG67	588263	2634	2 - 157	5321		H0181: 1				
HGBBG52	522424	2635	120 - 257	5322	Leu-8 to Gly-19, Leu-31 to Cys-36.	H0181: 1				
HGBBG38	525837	2636	1 - 150	5323	Ser-1 to Glu-10.	H0181: 1				
HGBBE12	971466	2637	1 - 69	5324		H0181: 1				
HGBBB78	773930	2638	1 - 342	5325	Ser-11 to Trp-17, Pro-19 to Thr-28.	H0181: 1 and L0741: 1.				
HBCPV80	932817	2639	2 - 403	5326	Arg-1 to Arg-8, Glu-29 to Arg-37.	AR061: 1, AR089: 1 H0663: 1 and L0783: 1.				
HBCPO75	927520	2640	135 - 356	5327	Ala-26 to Val-32.	L0779: 3, H0663: 1, L0757: 1 and L0758: 1.				
HBCPK03	922493	2641	194 - 514	5328	Lys-25 to Asn-34, Thr-92 to Gly-98.	H0663: 1 and L0766: 1.				
HBCJP02	917981	2642	349 - 507	5329	Glu-14 to Ala-30, Ile-46 to Lys-53.	H0664: 1 and L0758: 1.				
HBCJG07	951898	2643	3 - 137	5330	Arg-5 to Ser-15.	L0754: 2, H0664: 1 and L0748: 1.				
HAUCC58	764851	2644	31 - 402	5331	Cys-1 to Arg-15, Lys-28 to Asp-36.	H0294: 1 and L0777: 1.				



[066] The first column in Table 1A provides a unique "Clone ID NO:Z" for a cDNA clone related to each contig sequence disclosed in Table 1A. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods known in the art and/or as described elsewhere herein.

[067] The second column in Table 1A provides a unique "Contig ID" identification for each contig sequence. The third column provides the "SEQ ID NO:X" identifier for each of the reproductive system associated contig polynucleotide sequences disclosed in Table 1A. The fourth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A, column 5, as SEQ ID NO:Y. Where the nucleotide position number "To" is lower than the nucleotide position number "From", the preferred ORF is the reverse complement of the referenced polynucleotide sequence.

[068] The fifth column in Table 1A provides the corresponding SEQ ID NO:Y for the polypeptide sequence encoded by the preferred ORF delineated in column 4. In one embodiment, the invention provides an amino acid sequence comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by "ORF (From-To)". Also provided are polynucleotides encoding such amino acid sequences and the complementary strand thereto.

[069] Column 6 in Table 1A lists residues comprising epitopes contained in the polypeptides encoded by the preferred ORF (SEQ ID NO:Y), as predicted using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). In some embodiments, polypeptides of the invention comprise, or alternatively consist of, at least one, two, three, four, five or more of the predicted epitopes as described in Table 1A. It will be appreciated that depending on

the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly.

[070] Column 7 in Table 1A provides an expression profile and library code: count for each of the contig sequences (SEQ ID NO:X) disclosed in Table 1A, which can routinely be combined with the information provided in Table 4 and used to determine the normal or diseased tissues, cells, and/or cell line libraries which predominantly express the polynucleotides of the invention. The first number in column 7 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. For those identifier codes in which the first two letters are not "AR", the second number in column 7 (following the colon) represents the number of times a sequence corresponding to the reference polynucleotide sequence was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of <sup>33</sup>P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression. The sequences disclosed herein have been determined to be predominantly expressed in reproductive

system tissues, including normal and diseased reproductive system tissues (See Table 1A, column 7 and Table 4).

[071] Column 8 in Table 1A provides a chromosomal map location for certain polynucleotides of the invention. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Each sequence in the UniGene database is assigned to a "cluster"; all of the ESTs, cDNAs, and STSs in a cluster are believed to be derived from a single gene. Chromosomal mapping data is often available for one or more sequence(s) in a UniGene cluster; this data (if consistent) is then applied to the cluster as a whole. Thus, it is possible to infer the chromosomal location of a new polynucleotide sequence by determining its identity with a mapped UniGene cluster.

[072] A modified version of the computer program BLASTN (Altschul et al., J. Mol. Biol. 215:403-410 (1990), and Gish et al., Nat. Genet. 3:266-272 (1993)) was used to search the UniGene database for EST or cDNA sequences that contain exact or near-exact matches to a polynucleotide sequence of the invention (the "Query"). A sequence from the UniGene database (the "Subject") was said to be an exact match if it contained a segment of 50 nucleotides in length such that 48 of those nucleotides were in the same order as found in the Query sequence. If all of the matches that met this criteria were in the same UniGene cluster, and mapping data was available for this cluster, it is indicated in Table 1A under the heading "Cytologic Band". Where a cluster had been further localized to a distinct cytologic band, that band is disclosed; where no banding information was available, but the gene had been localized to a single chromosome, the chromosome is disclosed.

[073] Once a presumptive chromosomal location was determined for a polynucleotide of the invention, an associated disease locus was identified by comparison with a database of diseases which have been experimentally associated with genetic loci. The database used was the Morbid Map, derived from OMIM™ (*supra*). If the putative chromosomal location of a polynucleotide of the invention (Query sequence) was associated with a disease in the Morbid Map database, an OMIM reference identification number was noted in column 9, Table 1A, labeled "OMIM Disease Reference(s)". Table 5 is a key to the OMIM reference identification

numbers (column 1), and provides a description of the associated disease in Column 2.

**TABLE 1B**

Clone ID NO:Z	SEQ ID NO:X	CONTIG ID:	BAC ID: A	SEQ ID NO:B	EXON From-To
HAOSH55	14	952380	AL353194	5385	1-964 1250-1399 2650-2905 3588-3668 3971-4987 5854-5963 7336-7775 7870-8256 8419-8895 9000-9339
HAOSH55	14	952380	AL353194	5386	1-90
HAQAK73	15	764671	AC023906	5387	1-739
HAQAK73	15	764671	AC023906	5388	1-845
HAQBS37	20	847519	AP002519	5389	1-168 683-777 1538-3043 3578-4180 5564-5793 6266-6409 6412-6738 7035-7451
HAUBD69	21	529711	AL359674	5390	1-138
HAUBD69	21	529711	AL359674	5391	1-380
HAUBU10	22	968339	AC027538	5392	1-463
HAUBU10	22	968339	AC010770	5393	1-463
HAUBU10	22	968339	AC027538	5394	1-288
HAUBU10	22	968339	AC010770	5395	1-288
HBCQS93	27	930682	AL109945	5396	1-310 1220-1839
HBCQS93	27	930682	AC022307	5397	1-310 1220-1839 2206-2683 2691-2788 3337-3381
HBCQS93	27	930682	AL109945	5398	1-131
HBGBF56	29	957870	AL031963	5399	1-249
HBGBF56	29	957870	AL133351	5400	1-249
HBGBF56	29	957870	AL031963	5401	1-249
HBGBF56	29	957870	AL031963	5402	1-429
HBGBF56	29	957870	AL133351	5403	1-580 1364-1792 2134-2229 3072-3565



					3973-4080
HBGBF56	29	957870	AL031963	5404	1-349
HBGBF56	29	957870	AL133351	5405	1-349
HBGBF56	29	957870	AL031963	5406	1-349
HBGBG42	30	922396	AL096773	5407	1-518 1341-1514 3365-3956 4169-4282 4430-4892 6254-7763
HBGBG42	30	922396	AL096773	5408	1-114
HBGBG42	30	922396	AL096773	5409	1-3033
HBGBH43	31	524532	AP000757	5410	1-726
HBGBH43	31	524532	AP000683	5411	1-726
HBGBH43	31	524532	AP000757	5412	1-249 299-451 651-926
HBGBH43	31	524532	AP000683	5413	1-249 299-452 651-926
HBGBS07	32	954299	AL358472	5414	1-93 229-341 458-525 639-725 820-2416 3085-3172 3955-5506 5626-6422
HBGBS07	32	954299	AL358472	5415	1-391
HBGBS07	32	954299	AL358472	5416	1-344 399-469
HBGBW60	34	954916	AC007779	5417	1-542 1709-1905 3246-3805
HBGBW60	34	954916	AC015667	5418	1-542 1705-1901 3242-3801
HBGBW60	34	954916	AC007936	5419	1-545 1736-1917 3269-3833 6267-6287
HBGBW72	35	524956	AL139376	5420	1-448
HBGBW72	35	524956	AL139376	5421	1-526
HBGDE85	37	524875	AC020850	5422	1-912 1276-1413
HBGDE85	37	524875	AC008693	5423	1-138
HBGDE85	37	524875	AC023611	5424	1-105

HBGDE85	37	524875	AC022123	5425	1-957 1332-1469
HBGDE85	37	524875	AC010845	5426	1-138
HBGDT43	39	974223	L81574	5427	1-168
HBGDT43	39	974223	AC022276	5428	1-166
HBGDT43	39	974223	AC023653	5429	1-57
HBGDT43	39	974223	AC012102	5430	1-140
HBGDT43	39	974223	AC048382	5431	1-115
HBGDT43	39	974223	AC011036	5432	1-193
HBGDT43	39	974223	AC068682	5433	1-153
HBGDT43	39	974223	AL356496	5434	1-35
HBGDT43	39	974223	AC006087	5435	1-129
HBGDT43	39	974223	AC016142	5436	1-150
HBGDT43	39	974223	AC027456	5437	1-98
HBGDT43	39	974223	AC016797	5438	1-116
HBGDT43	39	974223	AL356606	5439	1-87
HBGDT43	39	974223	AC025181	5440	1-159
HBGDT43	39	974223	AC055788	5441	1-170
HBGDT43	39	974223	AC027264	5442	1-147
HBGDT43	39	974223	AC026537	5443	1-132
HBGDT43	39	974223	AC000360	5444	1-142
HBGDT43	39	974223	AC023583	5445	1-153
HBGDT43	39	974223	AL161613	5446	1-63
HBGDT43	39	974223	AC062010	5447	1-155
HBGDT43	39	974223	AC004803	5448	1-154
HBGDT43	39	974223	AC023583	5449	1-59 1391-1548
HBGDT43	39	974223	AL161613	5450	1-129
HBGDT43	39	974223	L81574	5451	1-315 1979-2215 2720-3771
HBGDT43	39	974223	AL356496	5452	1-131
HBGFA62	40	954306	AC016889	5453	1-700 855-956 962-1444 1446-2545 2846-3201 3316-3569 4130-4421 4424-4461
HBGFA62	40	954306	AC016889	5454	1-35 309-427 1161-1286 3151-3255 3263-3604 4836-5346

					5473-5765 6231-6283 6387-6534
HBGMD62	42	933763	AL031258	5455	1-692 707-1312
HBGMD62	42	933763	AC068332	5456	1-671
HBGMD62	42	933763	AL031258	5457	1-349 438-545 675-725 744-903 1124-1593 1726-1832 1904-1966 2656-2704
HBGMF10	43	966132	AC068259	5458	1-743 914-1113 1118-1586
HBGMF10	43	966132	AC068259	5459	1-466
HBGMF10	43	966132	AC068259	5460	1-279
HBGMZ39	45	947112	AC008537	5461	1-1186
HBGMZ39	45	947112	AC019337	5462	1-1182
HBGMZ39	45	947112	AC008537	5463	1-1993 2105-2385 2736-3068 4364-4489 6546-6781 7025-8165
HBGMZ39	45	947112	AC019337	5464	1-1991 2103-2383 2734-3066 4360-4485 6541-6776 7021-8159
HBGMZ39	45	947112	AC008537	5465	1-734 767-1001
HBGMZ39	45	947112	AC019337	5466	1-158 291-565 598-832
HBGND09	47	848219	AL139288	5467	1-1670
HBGND09	47	848219	AC023889	5468	1-1670
HBGND09	47	848219	AC026657	5469	1-1477
HBGND09	47	848219	AC023889	5470	1-440
HBGND09	47	848219	AL139288	5471	1-397
HBGND09	47	848219	AC026657	5472	1-396
HBGND09	47	848219	AC023889	5473	1-396
HBGNJ14	48	914594	AC004156	5474	1-56 391-1058

					1079-1478 1996-2053 2539-2612 2844-3219 3313-3602 3796-3919 4012-4767
HBGNJ14	48	914594	AC004156	5475	1-275
HBGNO07	50	952212	AC073131	5476	1-1122
HBGNO07	50	952212	AC008403	5477	1-1630 2058-2480 4161-4577 5334-5745 6732-6865 7024-7163 10746-11227 11908-12229 12481-13862
HBGNO07	50	952212	AC008403	5478	1-482 2074-2191 3067-3427 3514-3666 4176-4250 4718-4839 5313-5692 10395-10491 10694-10779 11107-11256 12127-12209 12283-12405 12543-13031 13771-14040
HBGNO07	50	952212	AC008403	5479	1-128 172-232 1302-2232
HBGNQ31	51	887152	AL118522	5480	1-258 787-912 2028-2776 3673-3948 4188-4463
HBGNQ31	51	887152	AL118522	5481	1-1160
HBGNW29	52	969396	AL139288	5482	1-1670
HBGNW29	52	969396	AC023889	5483	1-1670
HBGNW29	52	969396	AC026657	5484	1-1477
HBGNW29	52	969396	AC023889	5485	1-440
HBGNW29	52	969396	AL139288	5486	1-397
HBGNW29	52	969396	AC026657	5487	1-396

HBGNW29	52	969396	AC023889	5488	1-396
HBGOB07	53	883111	AC008655	5489	1-895
HBGOB07	53	883111	AC008655	5490	1-1013
HBGOB07	53	883111	AC008655	5491	1-909 1371-1545 3390-3501 4360-4549 5287-5337 5422-5540 7645-7790 8678-8898 9930-10085
HBGPH02	58	918513	AC003037	5492	1-492
HBGPH02	58	918513	AC003037	5493	1-86 3463-3839 4494-4881 4901-6058
HBGPH02	58	918513	AC003037	5494	1-2178 2394-3039 3041-3358 4072-4175 4212-4316 4571-4941 5381-5529 5783-5886 6445-6588 8722-8835
HBGPK33	59	973425	AC012305	5495	1-712
HBGPK33	59	973425	AC067853	5496	1-712
HBGPK33	59	973425	AC067853	5497	1-601
HBGPV05	60	930706	AC020866	5498	1-592
HBGSD40	62	923142	AC007783	5499	1-215 697-1759
HBGSD40	62	923142	AC022007	5500	1-555
HBGSD40	62	923142	AC018809	5501	1-867
HBGSD40	62	923142	AC007783	5502	1-534
HBGSD40	62	923142	AC007783	5503	1-314 814-969 1228-1301 1391-1502 2374-2548 2750-3470
HBGSD40	62	923142	AC022007	5504	1-279
HBGSD40	62	923142	AC022007	5505	1-314 814-969 1228-1301 1391-1502

					2374-2548 2750-3492 3815-3858 4506-4812 5780-6087 6765-6905 7117-7178 11051-11101 11244-11380 11469-11524 12621-12789 12919-13141 13291-13351 13474-13835 14502-14734 14773-15067 15215-16491
HBGSD40	62	923142	AC018809	5506	1-314 814-969 1228-1301 1391-1502 2375-2549 2751-3431
HBGTL01	64	914573	Z97986	5507	1-696 3066-3591
HBGTL01	64	914573	Z97986	5508	1-334
HBANAN41	69	655842	AC005729	5509	1-307
HBANAN41	69	655842	AC005729	5510	1-116
HBANAN41	69	655842	AC005729	5511	1-177
HBANAX71	71	530843	AL157375	5512	1-87
HBANAX71	71	530843	AL157375	5513	1-430
HBANAY58	72	558193	AC046185	5514	1-836
HBNBT52	73	524869	AC069303	5515	1-488
HBNBT52	73	524869	AC069303	5516	1-205
HBNBT52	73	524869	AC069303	5517	1-315
HBZAJ09	74	655769	AC019232	5518	1-315
HBZAJ09	74	655769	AC025171	5519	1-315
HBZAJ09	74	655769	AC019232	5520	1-324
HBZAJ09	74	655769	AC025171	5521	1-148
HBZAJ09	74	655769	AC019232	5522	1-148
HBZAJ09	74	655769	AC025171	5523	1-283
HBZSH16	75	655619	AC069483	5524	1-554
HBZSH16	75	655619	AC069483	5525	1-920
HBZSH71	76	760418	AC018693	5526	1-741
HBZSH71	76	760418	AC018693	5527	1-252
HBZSI73	77	655737	AC067954	5528	1-313
HBZSI73	77	655737	AC067954	5529	1-326

HBZSK17	78	664013	AC005005	5530	1-139 521-674 838-1409 1438-1598 1860-1995 6648-6796 7196-7292 7385-7460 7554-7650 8380-8713 8789-8863 9491-9560 9642-9826 10042-10528 11147-11210 13983-15090 15211-15587 15681-16021 17348-17536 17744-17862 17957-18234 18373-18580 19081-19435 19568-19733 19815-19932 20132-20466 22166-22791 22824-23307
HBZSK17	78	664013	AC005005	5531	1-1393 2604-2971
HCBMV01	79	914333	AP002479	5532	1-401
HCBMV01	79	914333	AC012569	5533	1-193 379-463 1042-1115 2571-3004 3344-3468 4339-4433 5418-5606 5875-6012 6119-6519 7622-7713
HCBMV01	79	914333	AP001895	5534	1-74 1527-1591 1656-1960 2300-2424 3295-3389 4374-4562

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HCBMV01	79	914333	AP002479	5535	1-189
HCBMV01	79	914333	AC012569	5536	1-87
HCBMV01	79	914333	AP001895	5537	1-87
HCBMV01	79	914333	AP001895	5538	1-108
HCBNW02	80	950897	AF205589	5539	1-32 110-254 333-849 918-999 1069-1147 1231-1322 1435-1687 1765-1881 1958-2357 2441-3044 3104-3153 3226-3549 3626-3791 3874-4018 4089-4184 4258-4377 4424-5493 5591-5736 5834-5922 6196-6415 6479-6654 6735-6895 7030-7124 7229-7371 7452-7567 7707-7796 7887-7969 8059-8133 8149-8306 8381-8736
HCDMB01	83	915613	AC012484	5540	1-355
HCDMC01	86	915239	AC005789	5541	1-48 1051-2390 2839-3458
HCDMC01	86	915239	AC005789	5542	1-1721 2187-3101 3194-3363 4200-4903 5310-5493 6194-6294



					7366-7482 7598-7676 8092-8778 8869-9496
HCDMD23	87	676799	AC018743	5543	1-801
HCDMD23	87	676799	AC018630	5544	1-413
HCDMD23	87	676799	AC018743	5545	1-138
HCDMD23	87	676799	AC018630	5546	1-177
HCHAD40	88	923764	AC006096	5547	1-240 737-1362
HCHAD40	88	923764	AC006106	5548	1-240 736-1423
HCHAD40	88	923764	AC006108	5549	1-240 736-1359
HCHAD40	88	923764	AC006179	5550	1-230 1021-1223
HCHAD40	88	923764	U82205	5551	1-255 736-849 1023-1457
HCHAD40	88	923764	U82208	5552	1-240 736-1425
HCHAD40	88	923764	AC006186	5553	1-2213 2217-2456 2952-4550 4562-4643 4906-5701
HCHAD40	88	923764	AC006171	5554	1-240 736-1540 7244-8075 8087-8167
HCHAD40	88	923764	AC006177	5555	1-2212 2216-2455 2951-4547 4559-4639 4902-5697
HCHAD40	88	923764	AC006180	5556	1-240 736-1625
HCHAD40	88	923764	U82210	5557	1-2210 2214-2453 2949-4547 4559-4614 4899-5620
HCHAD40	88	923764	AC006185	5558	1-240 736-1359
HCHAD40	88	923764	AC006184	5559	1-2204 2208-2447 2943-3574

					3724-4540 4552-4633 4896-5715
HCHAD40	88	923764	AC006172	5560	1-240 847-1425
HCHAD40	88	923764	AC006099	5561	1-240 736-1424
HCHAD40	88	923764	AC006103	5562	1-240 737-2325
HCHAD40	88	923764	AC006098	5563	1-240 736-1424
HCHAD40	88	923764	AC006096	5564	1-2211
HCHAD40	88	923764	AC006106	5565	1-2215
HCHAD40	88	923764	AC006108	5566	1-2210
HCHAD40	88	923764	AC006179	5567	1-358
HCHAD40	88	923764	U82205	5568	1-2213
HCHAD40	88	923764	U82208	5569	1-2212
HCHAD40	88	923764	AC006171	5570	1-2213
HCHAD40	88	923764	AC006177	5571	1-67 1558-1614 1692-2134 2610-2767 4075-4344 5072-5484 5971-6837 7042-7752
HCHAD40	88	923764	AC006180	5572	1-2213
HCHAD40	88	923764	AC006171	5573	1-794
HCHAD40	88	923764	AC006185	5574	1-2206
HCHAD40	88	923764	AC006184	5575	1-130
HCHAD40	88	923764	AC006172	5576	1-2211
HCHAD40	88	923764	AC006099	5577	1-2212
HCHAD40	88	923764	AC006103	5578	1-2213
HCHAD40	88	923764	AC006098	5579	1-2212
HCHAR16	89	675465	AC068327	5580	1-402 667-3113
HCHAR43	90	715128	AC003036	5581	1-444 4270-4530 7834-7966 8367-8509 9404-9466 9576-9674
HCHAR43	90	715128	AC003036	5582	1-550
HCHBQ03	92	923763	AC006106	5583	1-240 736-1423
HCHBQ03	92	923763	U82205	5584	1-255 736-849

					1023-1457
HCHBQ03	92	923763	U82208	5585	1-240 736-1425
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HTENY44	1842	870588	AC027544	8663	1-197 710-864 1263-1380 2382-2706 3184-3394 3970-4082
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HTENV06	1843	933294	AL121753	8666	1-498
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HTENL95	1848	795314	AC022930	8670	1-32 79-745 880-1680 1782-2276 2861-3730 4861-5265
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HTELV29	1861	806421	AC068938	8696	1-643
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HTEJB07	1874	953801	AC073625	8714	1-494 2402-2532
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HTEIS34	1875	887112	AC069257	8718	1-635 725-895 1011-1169

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HTEHS17	1887	664436	AC010255	8734	1-184 308-529 2761-3109
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HTEDX39	1909	530201	AC005726	8785	1-257
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HTEDX03	1911	925353	AC005300	8790	1-202
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HTEDW96	1912	881958	AC017028	8793	1-477 786-1004
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HTEDW59	1913	530448	AC025868	8795	1-217
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HTEDV86	1914	785818	AL356801	8797	1-763
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HTEDO75	1918	767024	AL049541	8799	1-910
HTEDJ92	1920	522827	AL390815	8800	1-295
HTEDI01	1923	961028	AC019205	8801	1-224
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HTEDH06	1929	869427	AC006251	8806	1-718 767-1512 1639-2023 2398-2655 2926-2990 3300-3357 4357-4395 5163-5275 5927-6337 6945-7074 7156-7444
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HTEDF22	1935	908406	AL138891	8813	1-822
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HTECE31	1941	508104	AC069360	8828	1-283
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HTECC45	1950	508124	AC034305	8852	1-320
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HPWDE86	1986	785710	AC021124	8909	1-1473 1741-2513 2636-3258 3403-3998 5728-6283 6454-6541 6613-7768 8422-8995 9025-9187 9699-10397 11541-11606 11644-11887 13552-14227 14437-15311 15960-16131 17491-17894 17906-18148 18243-20300
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HPWDE86	1986	785710	AC008821	8911	1-1473 1741-2513 2636-3258 3403-3998 5729-6284 6455-6542 6614-7768 8422-8995 9025-9187 9699-10397 11540-11605

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HPRTI16	2004	667652	AL109928	8957	1-200
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HODFD73	2343	909812	AL050332	9581	1-187 311-458 667-1020 2447-2586
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HODEA14	2351	859375	AC004821	9601	1-100 2352-2466 2802-2941 2960-3163 4980-5083 6842-6968 8774-9008 10405-10540 11412-11517 11577-11682 13279-13409
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HCBMZ07	2589	951788	AL049610	10076	1-37 1329-3923
HCBMY10	2590	961718	AL158048	10077	1-1688 1805-2714
HCBMY10	2590	961718	AC041046	10078	1-908
HCBMY10	2590	961718	AC041046	10079	1-112
HCBMY10	2590	961718	AL158048	10080	1-112
HCBMY10	2590	961718	AC041046	10081	1-703
HCBMG11	2591	965394	AC013669	10082	1-181 291-782 2171-2360 2703-3570 4336-4689 5249-5785 5817-6442 6834-7458
HCBMG11	2591	965394	AC013669	10083	1-487
HBZSG02	2593	920249	AC008053	10084	1-996
HBZSG02	2593	920249	AC008053	10085	1-112
HBZSD32	2594	699335	AC011235	10086	1-354
HBZSD32	2594	699335	AC011235	10087	1-151
HBZAJ73	2595	764479	AC073594	10088	1-729 1248-1374
HBZAJ73	2595	764479	AC068986	10089	1-729 1248-1375
HBZAJ73	2595	764479	AC010892	10090	1-729 1248-1375
HBZAJ73	2595	764479	AC073594	10091	1-555
HBZAJ73	2595	764479	AC068986	10092	1-554
HBZAJ73	2595	764479	AC010892	10093	1-554
HBZAJ26	2596	681879	AC036116	10094	1-682
HBZAJ26	2596	681879	AL358976	10095	1-682
HBZAJ26	2596	681879	AC036116	10096	1-245 1588-2237
HBZAJ26	2596	681879	AL358976	10097	1-689
HBZAJ26	2596	681879	AC036116	10098	1-689
HBZAJ26	2596	681879	AL358976	10099	1-245 1588-2237
HBZAI39	2597	847621	AC009036	10100	1-1337
HBZAI39	2597	847621	AC012320	10101	1-1338

HBZAI39	2597	847621	AC009036	10102	1-126
HBZAI39	2597	847621	AC009036	10103	1-104
HBZAI14	2598	847620	AC073635	10104	1-466
HBZAI14	2598	847620	AC073635	10105	1-676
HBZAB15	2599	660348	AC019190	10106	1-894 941-2689
HBZAB15	2599	660348	AC025171	10107	1-894 941-2485
HBZAB08	2600	959560	AP002448	10108	1-235
HBZAB08	2600	959560	AP002448	10109	1-272
HBNBL29	2603	703113	AC008915	10110	1-1744
HBNBL29	2603	703113	AC008915	10111	1-420
HBNBJ29	2604	907015	AC036160	10112	1-334
HBNBJ29	2604	907015	AC016995	10113	1-334
HBNBJ29	2604	907015	AC036160	10114	1-470
HBNBJ29	2604	907015	AC036160	10115	1-99
HBNBJ29	2604	907015	AC016995	10116	1-99
HBNBJ29	2604	907015	AC016995	10117	1-470
HBNBJ06	2605	960664	AC061996	10118	1-527
HBNBJ06	2605	960664	AC022579	10119	1-173 1341-1867 4892-4933
HBNBJ06	2605	960664	AC022579	10120	1-492
HBNBB09	2608	868924	AL365223	10121	1-73 2336-3428
HBNBB09	2608	868924	AL365223	10122	1-851
HBNAW73	2609	764716	Z99289	10123	1-1491
HBNAW73	2609	764716	Z99289	10124	1-110
HBNAW73	2609	764716	Z99289	10125	1-190 1730-1923 2881-3366 4302-4465 4635-5036 6198-6347 6938-7175 7445-7543 7995-8128 12062-13446 13544-14273
HBNAAC32	2614	526549	AC018648	10126	1-855 1191-1323 3823-3881 4371-5379
HBNAAC32	2614	526549	AC018648	10127	1-125 180-388 891-1383 1802-1965

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HBNAC28	2615	525832	AC007539	10128	1-728
HBNAC09	2617	525833	AL132713	10129	1-2438
HBNAC09	2617	525833	AL132713	10130	1-355 392-835 914-995 1054-1333 1586-1743 2135-2199
HBNAC09	2617	525833	AL132713	10131	1-124
HBNAC02	2618	921187	AL133523	10132	1-188
HBNAC02	2618	921187	AL133523	10133	1-1700 1768-2230 2511-2678 3146-6917 8428-8644 8873-9205 11616-11679 14711-14834 15647-16163 17626-17691 18185-18607 20796-20845
HBNAC02	2618	921187	AL133523	10134	1-113 2404-2767 2862-3319 3371-3750 3847-4180 6007-6752 8810-9371
HBGTT76	2619	903653	AC006512	10135	1-658 3090-3543 4479-5105 5885-6846 7103-9707 9914-10293 11523-12034 12067-12181 13769-14031 14199-14291 14584-14790 15123-15154 17039-17482 17539-17987 18697-19052 19112-19380 20023-20268

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HBGTT76	2619	903653	AC006512	10136	1-315 439-531 707-1080 1144-1227 1491-1845 2113-2321 2700-3556 3818-4307 4336-4813 4958-5775
HBGTT76	2619	903653	AC006512	10137	1-738
HBGTE11	2620	965121	AF037222	10138	1-34 504-637 1210-2684 3241-3528 3799-4114 4225-4439 4754-4886 5520-6004 6811-6950 8255-8470 9691-10480 10798-11383 12144-12327 12452-12657 12889-13456 13751-13876 13921-14373 14745-15119 15895-16112

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HBGTE11	2620	965121	AL049840	10139	1-34 527-678 1208-2682 3785-4100 4211-4425 5506-5990 6797-6936 8241-8456 9677-10466 10784-11369 12130-12313 12438-12643 12875-13442 13740-13862 13907-14359 14731-15105 15881-16098 16275-16324 16440-17849
HBGTE11	2620	965121	AF037222	10140	1-126
HBGTE11	2620	965121	AF037222	10141	1-941 1055-1957
HBGTE11	2620	965121	AL049840	10142	1-126
HBGTE11	2620	965121	AL049840	10143	1-1797
HBGQS88	2621	886650	AC004152	10144	1-1226
HBGNL85	2622	848179	AL359510	10145	1-340 433-1692
HBGNL85	2622	848179	AL359510	10146	1-620
HBGND04	2623	926973	AC011686	10147	1-50 2676-3023 3161-3501 3760-4076 5867-6062 6851-7280 7581-8170
HBGND04	2623	926973	AP000560	10148	1-1137 1749-2085 4498-4845 4983-5323 5582-5898 7689-7884 8673-9102 9403-9993
HBGND04	2623	926973	AP001324	10149	1-50 2675-3022

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HBGND04	2623	926973	AP000560	10150	1-93
HBGND04	2623	926973	AC011686	10151	1-3688 3726-3971 4813-5933 6168-6648
HBGND04	2623	926973	AP001324	10152	1-2189
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HBGMT82	2624	954374	AP000449	10154	1-1171 1258-1698
HBGMT82	2624	954374	AC055871	10155	1-1174 1258-2167 2367-2591 2949-3669
HBGMT82	2624	954374	AJ002553	10156	1-286
HBGMT82	2624	954374	AC051660	10157	1-1173 1256-2164 2364-2588 2946-3665 3840-4059 4135-4280
HBGMT82	2624	954374	AJ002553	10158	1-137 586-767
HBGMT82	2624	954374	AC051660	10159	1-473
HBGMT82	2624	954374	AC051660	10160	1-82 433-487 583-1153 1232-1412
HBGMS69	2625	754392	AC010427	10161	1-757
HBGMS69	2625	754392	AC026740	10162	1-757
HBGMS69	2625	754392	AC016498	10163	1-757
HBGMS69	2625	754392	AC010427	10164	1-424
HBGMS69	2625	754392	AC026740	10165	1-115 765-1186
HBGMS69	2625	754392	AC010427	10166	1-416
HBGMS69	2625	754392	AC016498	10167	1-424
HBGMS69	2625	754392	AC026740	10168	1-227 229-411
HBGMS69	2625	754392	AC016498	10169	1-417
HBGMO78	2626	773043	AL139220	10170	1-877 1373-1821 2802-3760 3769-4392



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HBGMO78	2626	773043	AL357079	10171	1-878 1374-1822 2800-3758 3767-4390 4968-5660
HBGMO78	2626	773043	AC005038	10172	1-878 1374-1822 2803-3761 3770-4393 5226-5663 5775-5902 6120-6317 9252-9488 9701-10068 11666-11809
HBGMO78	2626	773043	AC005038	10173	1-1280 1472-1999 2116-3378
HBGMO78	2626	773043	AC005038	10174	1-1182 1260-1342 1447-2170 2566-3297 3550-3759 4478-4598 4690-4919 5109-5311
HBGMG81	2627	880276	AC026905	10175	1-38
HBGMG81	2627	880276	AC027551	10176	1-38
HBGMG81	2627	880276	AL365398	10177	1-47
HBGMG81	2627	880276	AC020714	10178	1-440 1153-1430
HBGMG81	2627	880276	AC006512	10179	1-247 2812-2918 3488-3953 3964-4527 4683-5151 5330-9121 9884-10335 10748-10781 10960-11055 11323-12111 12127-12791 12911-13262 13266-13791 14696-14866 15107-15207

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HBGMG81	2627	880276	AC027551	10180	1-131
HBGMG81	2627	880276	AC020714	10181	1-842
HBGMG81	2627	880276	AC006512	10182	1-818 963-1440 1469-1958 2220-3076 3455-3663 3931-4285 4549-4632 4696-5069 5245-5337 5461-5775
HBGMG81	2627	880276	AC020714	10183	1-1160
HBGMG81	2627	880276	AC006512	10184	1-738
HBGFS88	2628	914032	AC010687	10185	1-144 1186-2261
HBGFS88	2628	914032	AC005369	10186	1-649 870-1459 2153-2236 2499-2621 2722-2856 3368-3523 4084-4227 4315-4423 4652-4777 5094-5193 5519-5647 5739-5983

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HBGFS88	2628	914032	AC010687	10187	1-109
HBGFS88	2628	914032	AC005369	10188	1-109
HBGFS88	2628	914032	AC005369	10189	1-86 357-503
HBGFG53	2629	727748	AC026666	10190	1-791
HBGFG53	2629	727748	AC026283	10191	1-1463
HBGFG53	2629	727748	AC026666	10192	1-244
HBGFG53	2629	727748	AC026283	10193	1-319
HBGFG53	2629	727748	AC026283	10194	1-297 330-1653
HBGDA74	2632	832888	AP001100	10195	1-102 420-643 761-840 1681-1796 1917-2066 2158-2417 3079-3200 3281-3345 3436-4001 4062-4625
HBGDA74	2632	832888	AP000481	10196	1-64 188-337 429-688 1350-1471 1552-1616 1707-2271 2332-2895
HBGDA74	2632	832888	AP000481	10197	1-540 1012-1076 1166-1313 1698-1760 1787-1874 1971-2103 2575-2765 3027-3073
HBGDA74	2632	832888	AP001100	10198	1-540

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HBGBG52	2635	522424	AL136458	10199	1-294 506-707 1776-2011 2535-4755 5405-5870 5873-6187 7245-7361 7501-7967 9091-9694 9825-10069 10913-11066 11815-12127
HBGBG52	2635	522424	AC069042	10200	1-245
HBGBG52	2635	522424	AL162739	10201	1-245
HBGBG52	2635	522424	AL136458	10202	1-112
HBGBG52	2635	522424	AL162739	10203	1-604
HBGBB78	2638	773930	AC008403	10204	1-1630 2058-2480 4161-4577 5334-5745 6732-6865 7024-7163 10746-11227 11908-12229 12481-13862
HBGBB78	2638	773930	AC008403	10205	1-482 2074-2191 3067-3427 3514-3666 4176-4250 4718-4839 5313-5692 10395-10491 10694-10779 11107-11256 12127-12209 12283-12405 12543-13031 13771-14040
HBGBB78	2638	773930	AC008403	10206	1-128 172-232 1302-2232
HBCPO75	2640	927520	AC069279	10207	1-596 4098-4739 5478-5650

					6045-6577 6988-7374
HBCPK03	2641	922493	AC011719	10208	1-923
HBCPK03	2641	922493	AP001104	10209	1-923
HBCPK03	2641	922493	AP001324	10210	1-923
HBCJP02	2642	917981	AP000795	10211	1-935 1442-2055 2120-2651
HBCJP02	2642	917981	AC018775	10212	1-935 1442-2055 2120-2653
HBCJP02	2642	917981	AC011088	10213	1-254 1365-1474 2669-2833 3184-3483 3853-4390 9055-9989 10496-11109 11174-11705 14770-14905 15601-16949 24077-24508 25195-25367 27155-27556 28055-28776 29078-30192 35093-35409 37099-37222 37906-38308 39047-39871 40730-41079 41464-41939 42882-44161
HBCJP02	2642	917981	AC011088	10214	1-379
HBCJG07	2643	951898	AL158821	10215	1-179 415-1143
HBCJG07	2643	951898	AL158821	10216	1-401 691-974 1279-2180
HAUCC58	2644	764851	AC006329	10217	1-159 388-562 976-1372 1647-1772 1796-2110 2230-2442 3917-4291 4695-4807

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HAUCC58	2644	764851	AC006329	10218	1-338 1214-1745
HAUAS89	2646	518847	AC008044	10219	1-119 2461-2803 4346-4547 5141-5577 7669-7807 7933-8244 8849-8944 9208-10426 12618-12735 13747-14129 14744-15306
HAUAS89	2646	518847	AC008044	10220	1-55 3400-3593
HAUAS89	2646	518847	AC008044	10221	1-495
HAUAQ28	2647	685374	AC027523	10222	1-1260
HAUAQ28	2647	685374	AC011774	10223	1-1260
HAUAQ28	2647	685374	AP001848	10224	1-1260
HAUAQ28	2647	685374	AC027523	10225	1-535
HAUAQ28	2647	685374	AC011774	10226	1-535
HAUAQ28	2647	685374	AP001848	10227	1-535
HACMR08	2650	955638	AC012318	10228	1-147
HACMR08	2650	955638	AL121844	10229	1-219
HACMR08	2650	955638	AC013553	10230	1-280 2514-2880 3507-3803 5834-5958 8010-8114 9356-9430 13100-13296 14272-14676 14966-15305 15968-16340 16952-17049 17302-17464 18685-19018

					19824-20193 20412-20822 21304-21778 22964-23210 23327-23714 24031-24645 24690-24771 26370-27118
HACMR08	2650	955638	AL121656	10231	1-2346 2487-3703 3832-4167

[074] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

**TABLE 2**



Clone ID NO:Z	Contig ID:	SEQ ID NO:X	Analysis Method	PFam/NR Description	PFam/NR Accession Number	Score/ Percent Identity	NT From	NT To
H7MDD72	847688	13	blastx.2	(AF034780) lysophingolipid receptor Edg5 [Homo sapiens]	gb AAC98919.1	95%	597	7
H7MDD72	887805	2651	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin family)	PF00001	118	75	668
HAOSH55	952380	14	blastx.2	(AF200357) pantothenate kinase 1 beta [Mus musculus]	gb AAF23952.1 AF2 00357_1	78%	2	337
HAQAK73	764671	15	blastx.2	galactosylceramide-like protein, GCP - human	pir JC5238 JC5238	65%	129	7
HAQBJ71	839982	18	blastx.2	BasR [Escherichia coli]	dbj BAA03143.1	97%	127	2
HBCJS08	957826	23	blastx.2	(AK002129) unnamed protein product [Homo sapiens]	dbj BAA92096.1	51%	392	123
HBGBG42	922396	30	blastx.2	(AF161472) HSPC123 [Homo sapiens]	gb AAF29087.1 AF1 61472_1	66%	188	346
HBGBT79	525352	33	blastx.2	Invasin. [Escherichia coli]	dbj BAA15799.1	50%	85	315
HBGBW60	954916	34	blastx.2	paired-like homeodomain protein PRX2 [Homo sapiens]	gb AAB39864.1	58% 49% 87%	35 3 199	331 209 246
HBGDE85	524875	37	blastx.2	core protein [Escherichia coli]	gb AAA24544.1	100%	101	235
						90%	1	126

HBGDS13	971696	38	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	4.57	167	211
			blastx.2	rhaR (AA 1-312) [Escherichia coli]	emb CAA29453.1	86%	257	129
HBGDT43	974223	39	blastx.2	(AK000496) unnamed protein product [Homo sapiens]	dbj BAA91205.1	92%	141	100
						80%	445	311
HBGMD05	870189	41	blastx.2	Fos-related antigen [Rattus norvegicus]	gb AAA79137.1	88%	4	207
HBGMZ39	947112	45	HMMER 2.1.1	PFAM: Cytochrome P450	PF00067	59.5	509	372
			blastx.2	cytochrome P450 2B - green monkey	pir JT0676 JT0676	43%	563	372
						43%	299	168
						40%	165	121
HBGND09	848219	47	blastx.2	(AF156271) RING finger protein terf [Homo sapiens]	gb AAD40286.1	97%	2	367
HBGNM13	912730	49	blastx.2	(AE000420) putative regulator [Escherichia coli]	gb AAC76465.1	97%	188	75
HBGNO07	952212	50	blastx.2	(AK000496) unnamed protein product [Homo sapiens]	dbj BAA91205.1	81%	383	303
						33%	169	53
HBGNQ31	887152	51	blastx.2	(AF022821) putative potassium channel DP4 [Mus musculus]	gb AAD09338.1	56%	10	183
HBGPH02	918513	58	blastx.2	alpha 1C adrenergic receptor isoform 2 [Homo sapiens]	dbj BAA06901.1	71%	452	327
						93%	339	292
						69%	292	254

HBGPV05	930706	60	blastx.2	(AE000157) orf, hypothetical protein [Escherichia coli]	gb AAC73617.1	77%	617	36
HBGTR84	886529	65	blastx.2	(AL137718) hypothetical protein [Homo sapiens]	emb CAB70890.1	47%	555	346
HBNA Y58	558193	72	blastx.2	human elongation factor-1-delta [Homo sapiens]	emb CAA79716.1	76%	619	545
HCBNW02	950897	80	blastx.2	(AC008372) unknown [Homo sapiens]	gb AAF23326.1 AC008372.2	30%	21	581
HCBOG03	922351	82	HMMER 1.8	PFAM: Zinc finger, CCHC class	PF00098	73%	263	400
HCHAD40	923764	88	blastx.2	unidentified reading frame [Escherichia coli]	emb CAA23893.1	44%	1	270
HCHBQ03	923763	92	blastx.2	unidentified reading frame [Escherichia coli]	emb CAA23893.1	6.1	95	112
HCHND96	880585	94	blastx.2	(AF141920) roadblock [Drosophila melanogaster]	gb AAD45986.1 AF141920.1	85%	211	152
HCHOA76	740102	95	blastx.2	(AK000385) unnamed protein product [Homo sapiens]	dbj BAA91131.1	87%	311	264
HCHOD89	954866	96	blastx.2	cytochrome P450 2C34v2 [Sus scrofa]	gb AAA79105.1	100%	264	226
HCHQB06	934941	98	blastx.2	(AK001623) unnamed protein product [Homo sapiens]	dbj BAA91793.1	87%	325	302
HCOOZ11	965306	105	HMMER 1.8	PFAM: Src homology domain 3	PF00018	98%	334	158
						75%	174	455
						64%	499	335
						75%	266	195
						58%	336	286
						53%	94	189
						33%	6	86
						89%	183	440
						5.22	179	214

HEAAA42	963100	111	blastx.2 HMMER 1.8	(AL022238) dJ1042K10:2 (supported by GENSCAN, FGENES and GENEWISE) [Homo sapiens] PFAM: Zinc finger, C2H2 type	emb CAA18266.1	100%	182	589
			blastx.2	(AF117814) odd-skipped related 1 protein [Mus musculus]	gb AAD37115.1 AF1 17814_1	79%	18	221
HEEAH07	851219	124	blastx.2	(AL137469) hypothetical protein [Homo sapiens]	emb CAB70754.1	100%	178	270
HEEAJ58	785121	125	blastx.2	(AF080470) pallid [Homo sapiens]	gb AAF08343.1 AF0 80470_1	100% 100% 66%	169 90 169	258 170 252
HEEAJ76	887321	126	blastx.2	truncated protein [Saccharomyces cerevisiae]	gb AAB31222.1	87%	94	23
HEEAW01	851213	133	blastx.2	(AK000385) unnamed protein product [Homo sapiens]	dbj BAA91131.1	72%	371	210
HEGAB84	823900	137	HMMER 2.1.1	PFAM: Ank repeat	PF00023	36.9	205	315
			blastx.2	ankyrin 3 [Mus musculus]	gb AAB01605.1	37%	28	348
HEGA182	955291	140	blastx.2	putative [Rattus norvegicus]	emb CAA52297.1	58% 96% 31%	1 370 179	276 453 283
HEGAO83	780837	142	HMMER 1.8	PFAM: IG (immunoglobulin)	PF00047	9.4	234	305

HEGAZ61	950033	149	HMMER 2.1.1 blastx.2	superfamily PFAM: Reprolysin family propeptide	PF01562	141.4	276	560
HEPAB70	557149	151	blastx.2	epididymal apical protein I-precursor [Macaca fascicularis]	emb CAA46929.1	92%	60	560
HEPAP02	926914	160	blastx.2	ORF_ID:o209#7 [Escherichia coli]	dbj BAA35540.1	83% 87% 90%	99 43 326	329 141 355
HEPBA39	919875	163	HMMER 1.8 blastx.2	WW domain binding protein-1 [Homo sapiens] PFAM: lipocalins	gb AAD10950.1  PF00061	100% 26.73	59 117	163 509
HEPBH38	707524	169	blastx.2	(AF109472) epididymal protein 52 [Oryctolagus cuniculus]	gb AAC98311.1	42%	314	66
HEPCT32	947081	179	blastx.2	(AK000385) unnamed protein product [Homo sapiens]	dbj BAA91131.1	53%	319	146
HEPCU32	931824	180	HMMER 1.8 blastx.14	(AJ243311) matrix metalloproteinase-2 [Equus caballus] PFAM: lipocalins	emb CAB46656.1  PF00061	32% 39% 32% 27% 11.52	262 262 24 18 508	636 477 269 275 627
HEPCU32	946975	2652	HMMER	mE-RABP minor form protein [Mus musculus] PFAM: lipocalins	gi 3241966 gb AAC2 4316.1  PF00061	30% 20% 60% 11.52	502 336 279 405	630 482 308 524

			1.8					
			blastx.14	mE-RABP minor form protein [Mus musculus]	gi 3241966 gb AAC24316.1	30%	399	527
HEQAE65	911438	181	HMMER 2.1.1	PFAM: Myosin head (motor domain)	PF00063	35.1	50	148
			blastx.2	(AF234532) myosin X [Homo sapiens]	gb AAAF37875.1 AF234532.1	100%	2	154
HEQAH70	699690	182	blastx.2	(AJ007558) nucleoporin 155 [Homo sapiens]	emb CAA07553.1	85%	176	343
						97%	49	171
						65%	288	347
HEQAO76	769973	183	blastx.2	(AF053944) aortic carboxypeptidase-like protein ACLP [Homo sapiens]	gb AAC25585.1	100%	148	201
						100%	1	45
						34%	266	430
						34%	269	400
						31%	329	433
						36%	311	424
						24%	266	415
						57%	390	431
						35%	314	418
HETAF89	509300	189	blastx.2	(AF209069) hypothetical protein [Homo sapiens]	gb AAAF16744.1 AF209069.2	98%	72	248
HETAH66	799665	191	blastx.2	IgE-binding factor [Mus musculus]	gb AAA37291.1	57%	109	216
						37%	20	115
HETAZ13	536192	201	HMMER 1.8	PFAM: Src homology domain 3	PF00018	3.73	165	245
HETDI03	925489	217	blastx.2	zinc finger protein ZNF133 [Homo sapiens]	gb AAC50260.1	78%	18	131
						70%	15	134
						74%	15	131

HETDP21	525407	220	HMMER 1.8	PFAM: Zinc finger, C3HC4 type (RING finger)	PF00097	66% 73% 60% 71% 62% 64% 65%	18 18 18 18 18 18 18	143 131 146 131 146 134 140
HETFC82	799658	227	HMMER 1.8	(AF034745) LNXp80 [Mus musculus]	gb AAC40075.1	92% 61% 3.03	218 112 418	292 216 480
			blastx.2	PFAM: Bacterial mutT protein				
			blastx.2	(AL035291) hypothetical protein [Homo sapiens]	emb CAA22894.1	94%	7	531
HETFI24	954104	230	HMMER 1.8	PFAM: Spectrin alpha chain, repeated domain	PF00435	9.64	628	690
			blastx.2	myosin II heavy chain [Naegleria fowleri]				
HETFM43	973702	233	blastx.2	(AK002129) unnamed protein product [Homo sapiens]	dbj BAA92096.1	80% 53% 88%	200 303 268	262 347 294
			blastx.2	PFAM: IG (immunoglobulin) superfamily				
			HMMER 1.8	FOLLISTATIN-LIKE 2 (FOLLISTATIN-LIKE PROTEIN).	PF00047	15.57	213	392
HETGL74	947978	237	blastx.2		sp Q61581 Q61581	36%	132	440

HETHO63	745503	244	blastx.2	rhophilin [Mus musculus]	gb AAC52388.1	51%	160	450
HETHR24	851412	246	HMMER 2.1.1	PFAM: Fibrillar collagen C-terminal domain	PF01410	35%	47	157
HETIF01	966185	248	blastx.2	type V collagen [Gallus gallus]	gb AAB41274.1	53.4	201	308
HETIJ84	766589	250	blastx.2	fused-ccdB [Escherichia coli]	emb CAA71575.1	65%	213	308
HETJX04	927120	262	HMMER 2.1.1	(AF161432) HSPC314 [Homo sapiens]	gb AAF28992.1 AF1 61432_1	48%	86	214
HETJY11	966194	263	blastx.2	PFAM: C2 domain	PF00168	41%	336	437
HETKV26	910030	270	HMMER 2.1.1	(AB025258) granuphilin-a [Mus musculus]	dbj BAA84656.1	94%	122	223
HETKZ65	941045	272	blastx.14	(AK000496) unnamed protein product [Homo sapiens]	dbj BAA91205.1	57%	6	683
HLWAH41	944774	283	HMMER 2.1.1	PFAM: Oxysterol-binding protein	PF01237	48%	685	831
HLWAI13	920690	284	blastx.14	(AF067972) DNA cytosine methyltransferase 3 alpha [Homo sapiens]	gi 4927370 gb AAD3 3084.1 AF067972_1	70%	719	859
				PFAM: ENV polypeptide (coat polypeptide)	PF00429		3	227
				(AF108843) env protein [Homo sapiens]	gb AAD34324.1	84%	2	364
				(AL117538) hypothetical	gi 5912069 emb CAB	72%	63	500
						100%	455	520
						150	520	537
						50%	82	714
						100%	67	711
							496	588



HLWAJ64	746460	285	HMMER 1.8	protein [Homo sapiens] PFAM: Zinc finger, CCHC class	55984.1  PF00098	6.51	357	337
HLWAK69	694216	286	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	6.05	118	168
HLWAR77	947484	288	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin family)	PF00001	214.2	1287	553
			blastx.2	(AF119815) G-protein- coupled receptor [Homo sapiens]	gb AAD22047.1	99%	1287	292
HLWBQ84	782938	299	HMMER 1.8	PFAM: HMG (high mobility group) box	PF00505	9.46	21	110
HLWFG82	929647	317	HMMER 2.1.1	PFAM: Immunoglobulin domain	PF00047	32.6	121	330
			blastx.2	Frazzled [Drosophila melanogaster]	gb AAC47314.1	37% 43%	52 488	411 535
HNOAX12	969363	330	blastx.2	line-1 reverse transcriptase [Homo sapiens]	gb AAC51337.1	41%	710	465
HODAG37	529410	339	blastx.2	(AC004416) WUGSC:H_RG013N12.g w.1335199.a gene product [Homo sapiens]	gb AAC06181.1	54% 58%	229 137	131 87
HODBT58	678444	355	blastx.2	(AF118086) PRO1992 [Homo sapiens]	gb AAF22030.1 AF1 18094_25	69%	1	129
HODCV09	973487	375	blastx.2	(AF034209) RIG-like 5-6 [Homo sapiens]	gb AAB92665.1	100%	130	207
HODDQ21	919295	392	blastx.2	(AF161393) HSPC275	gb AAF28953.1 AF1	96%	3	245

HODDS67	567197	394		blastx.2	[Homo sapiens] (AK001614) unnamed protein product [Homo sapiens]	61393 1 dbj BAA91790.1	100% 100%	69 14	164 67
HODER91	789661	419		HMMER 1.8 blastx.2	PFAM: Zinc finger, C2H2 type (AC007059) Human homolog of Mus musculus wizL protein [AA 4-1561] [Homo sapiens]	PF00096 gb AAD19818.1	11.06 35%	163 1	225 294
HODEX10	926260	423		HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	9.2	22	54
HODFQ06	934304	451		blastx.2	(AK00496) unnamed protein product [Homo sapiens]	dbj BAA91205.1	48% 60%	466 537	254 454
HODFY16	958329	459		HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	3.15	175	213
HODGC61	973449	463		HMMER 1.8	PFAM: Protein-tyrosine phosphatase	PF00102	6.61	130	222
HODGH02	917969	465		blastx.2	IDN4-GGTR14 PROTEIN.	sp Q9Y6Y5 Q9Y6Y5	94%	17	118
HODGH04	926255	466		blastx.2	IDN4-GGTR14 PROTEIN.	sp Q9Y6Y5 Q9Y6Y5	51%	8	247
HODGI67	974297	471		blastx.14	pol gene protein; Xxx [Homo sapiens]	gi 1196424 gb AAA8 8026.1	70%	132	284
HODGP95	908650	477		HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	18.49	209	271

			blastx.2	(AC005498) R31665_1 [Homo sapiens]	gb AAC32422.1	61% 52% 53% 41% 34% 50% 51% 46% 47% 47% 47% 50% 35% 41%	125 146 146 125 74 146 164 164 307 307 307 310 307 307	310 310 292 310 334 307 310 310 357 357 357 357 357 357
HODGQ22	974290	479	blastx.2	hypothetical protein Tigger 2 - human transposon MER37.1	pir S72489 S72489	47% 57%	235 287	2 231
HODGQ92	894368	481	HMMER 2.1.1	PFAM: RhoGAP domain	PF00620	30.1	2	124
			blastx.2	(AC002398) F25965_3 [Homo sapiens]	gb AAB81198.1	63% 72%	142 2	399 133
HOFAD05	932211	507	blastx.14	unknown [murine herpesvirus 68]	gi 2318003 gb AAB6 6461.1	39% 45% 85%	263 192 120	180 127 100
HOFMB78	572941	512	HMMER 1.8	PFAM: Laminin B (Domain IV)	PF00052	1.62	286	330
			blastx.2	ribosomal protein L7a large subunit [Homo sapiens]	gb AAA60282.1	72% 61% 50%	49 236 44	399 397 91

HOFMF03	924679	516	blastx.2	U88 [Human herpesvirus 6]	emb CAA58337.1	54%	298	116
						49%	298	116
						50%	295	116
						51%	295	116
						54%	298	116
						50%	295	116
						51%	289	116
						55%	298	116
						48%	295	116
						46%	295	116
						52%	298	116
						48%	289	116
						43%	295	116
						51%	295	116
						49%	298	116
						45%	295	116
						43%	295	116
						46%	295	116
						45%	295	116
						54%	297	115
						43%	295	116
						43%	295	116
						45%	295	116
						46%	295	116
						44%	289	116
						44%	289	116
						43%	295	116
						44%	289	116
						46%	289	116
						43%	295	116

[illegible]

HOFMJ44	719663	525	HMMER 2.1.1	PFAM: Ribosomal protein S27	PF01667	38%	35	88
			blastx.2	(AF070668) 40S ribosomal protein S27 isoform [Homo sapiens]	gb AAD20974.1	109.1	128	265
HOFMM72	464015	528	blastx.2	(AL117557) hypothetical protein [Homo sapiens]	emb CAB55992.1	95%	56	274
HOFMP79	775242	531	HMMER 2.1.1	PFAM: GrpE	PF01025	65%	61	366
			blastx.2	mt-GrpE#1 precursor [Rattus norvegicus]	gb AAC53534.1	49.4	173	358
HOFMQ65	789347	534	blastx.2	(AL050369) hypothetical protein [Homo sapiens]	emb CAB43677.1	73% 86%	173 36	400 164
HOFMS89	575820	537	blastx.2	(AF161359) HSPC096 [Homo sapiens]	gb AAF28919.1 AFI 61359_1	68% 100% 64%	113 43 354	343 147 404
						53% 46% 69% 72%	181 71 411 48	411 277 488 80
HOFMT43	811542	539	blastx.2	glucosephosphate isomerase [Sus scrofa]	emb CAA82246.1	50% 80% 40%	143 57 277	514 161 501
HOFMT72	563575	541	blastx.2	Huntington Disease (HD) gene exon 1 [Homo sapiens]	emb CAA92991.1	82% 50%	52 297	2 256
HOFMU63	744325	543	blastx.2	(AK000334) unnamed protein product [Homo sapiens]	dbj BAA91091.1	63%	9	245
HOFNA92	792734	547	blastx.2	(AL109701) C15orf3	emb CAB52022.1	60%	151	339

HOFNG06	935569	556			[Homo sapiens]					emb CAB63728.1	86% 37% 33%	60 128 128	125 301 334
HOFNI08	974435	558			(AJ224442) methyltransferase [Homo sapiens]	blastx.2				emb CAA11944.1	90% 90% 100% 81%	80 66 253 25	241 95 270 423
HOFNLI8	666498	561			PFAM: Bacterial mutT protein	HMMER 1.8				PF00293	4.34	286	345
HOFNLI25	916963	562			PFAM: Ribosomal L18ae protein family	HMMER 2.1.1				PF01775	250.8	62	331
					ribosomal protein L18a - rat	blastx.2				pir S03957 R5RT18	73%	47	514
HOFNLI37	906250	563			vimentin [Mus musculus]	blastx.2				dbj BAA19834.1	51% 41% 100%	204 175 140	377 396 178
HOFNT59	615305	567			(AB026125) ART-4 [Homo sapiens]	blastx.2				dbj BAA86961.1	59% 42%	146 18	451 479
HOFNU72	705435	568			(AF086708) 26S proteasome subunit 11 [Homo sapiens]	blastx.2				gb AAC64104.1	94% 95% 81%	46 200 261	204 259 308
HOFNW79	973351	570			(AJ388527) Ribosomal protein [Canis familiaris]	blastx.2				emb CAB46829.1	96% 100% 84% 38%	85 276 365 80	273 362 403 133
HOFNY50	715312	572			(AF047704) tuftelin [Mus musculus]	blastx.2				gb AAC04577.1	92% 81%	224 127	388 222

HOFOB88	751692	579	blastx.2	(AF139185) myomegalin [Rattus norvegicus]	gb AAD29427.1	68%	69	143
HOFOB91	827631	580	blastx.2	nucleobindin [Homo sapiens]	gb AAA36383.1	90%	393	425
HOFOF57	666909	582	blastx.2	T28D6.9 [Caenorhabditis elegans]	emb CAB54316.1	58%	427	477
HOGAF39	947431	584	blastx.14	cyclin A/CDK2- associated p45 [Homo sapiens]	gi 995826 gb AAC50 242.1	80%	13	369
HOGCX95	890607	591	HMMER 1.8	PFAM: Retroviral aspartyl proteases	PF00077	86%	87	233
HOGEE76	968956	592	blastx.14	No definition line found [Caenorhabditis elegans]	gi 1397275 gb AAB0 3138.1	85%	23	43
HOVB Y34	706816	602	blastx.2	(AK002129) unnamed protein product [Homo sapiens]	dbj BAA92096.1	43%	141	347
HOVCD39	705406	605	blastx.2	(AF118081) PRO1900 [Homo sapiens]	gb AAF22025.1 AF1 18094 20	57%	347	388
HOVEK70	909138	615	HMMER 2.1.1	PFAM: Zinc finger, C2H2 type	PF00096	47%	78	179
			blastx.2	Bowel [Drosophila melanogaster]	gb AAB17949.1	45%	2	73
						42%	216	257
						32.8	205	504
						36%	650	790
						60%	599	643
						27%	500	586
						80%	177	40
						70%	20	151
						68.7	225	293
						88%	93	377
						35%	111	431
						34%	132	377
						85%	2	82
						32%	81	209



HPDOT03	922481	635	blastx.14	(AF061346) Edp1 protein [Mus musculus]	gi 3114713 gb AAC7 8826.1	33%	368	457
HPDPJ69	966158	637	blastx.14	envelope protein [Homo sapiens]	gi 1196425 gb AAA8 8027.1	61%	212	382
HPDRG92	967704	643	blastx.14	2-oxoglutarate dehydrogenase precursor [Homo sapiens]	gi 531241 dbj BAA01 393.1	53%	92	226
						62%	13	108
						82%	7	234
						73%	237	326
						35%	1	60
						75%	279	302
HPEKG18	914115	656	blastx.14	(AB012223) ORF2 [Canis familiaris]	gi 2981631 dbj BAA2 5253.1	75%	96	10
HPFEA08	960372	700	HMMER 1.8	PFAM: HMG (high mobility group) box	PF00505	5.1	68	148
HPIAS40	928614	708	blastx.14	(AF044954) NADH:ubiquinone oxidoreductase PDSW subunit [Homo sapiens]	gi 4164442 gb AAD0 5419.1	96%	68	232
						88%	304	384
						92%	262	303
						53%	384	461
HPIAX11	925424	710	blastx.2	(AL031427) dJ167A19.1 (novel protein) [Homo sapiens]	emb CAB46721.1	63%	342	569
						78%	449	604
HPIAZ37	655753	711	HMMER 1.8	PFAM: ATP synthase A chain	PF00119	11.95	68	238
HPIBQ37	884289	712	HMMER 2.1.1	PFAM: Immunoglobulin domain	PF00047	42	149	355
			blastx	(AF111713) junctional adhesion molecule [Homo sapiens]	gb AAD42050.1 AF1 11713_1	100%	89	385
						84%	385	423
HPJCC04	926787	731	blastx.14	(AF159714) PPAR gamma coactivator-1	gi 5802182 gb AAD5 1615.1 AF159714_1	94%	249	40

HPJDA08	958182	741	blastx.14	[Homo sapiens] zinc finger 5 protein [Gallus gallus]	gi 1399185 gb AAB3 8387.1	39%	92	475
HPJET90	836503	750	HMMER 2.1.1	PFAM: Aldehyde dehydrogenase family	PF00171	150.4	66	371
HPMEG50	925080	806	blastx.14	Mst84Dc [Drosophila melanogaster]	gi 11075 emb CAA47 939.1	62% 28% 44%	7 22 126	30 105 152
HPMFL08	959569	819	HMMER 1.8	PFAM: Src homology domain 3	PF00018	4.97	209	238
HPMGF06	954823	845	blastx.14	GTP binding protein [Mus musculus]	gi 53169 emb CAA36 803.1	92%	37	564
HPMGI03	924521	848	blastx.14	(AF106933) plexin B [Drosophila melanogaster]	gi 4056676 gb AAD0 9426.1	36% 60% 63% 43% 66%	49 148 12 288 359	147 177 44 335 385
HPMGX23	575903	864	HMMER 1.8	PFAM: Helix-loop-helix DNA-binding domain	PF00010	6.66	96	194
HPMJF76	965642	875	blastx.14	pol protein [Human endogenous retrovirus K]	gi 1780973 emb CAA 71417.1	58% 40% 63%	234 28 134	326 138 199
HPMJN59	946876	877	HMMER 1.8	PFAM: Prolyl oligopeptidase family	PF00326	21.87	138	251
			blastx.2	(AC005594) R26984_1 [Homo sapiens]	gb AAC33801.1	61%	138	521
HPMKM81	894416	884	HMMER 2.1.1	PFAM: Homeobox domain	PF00046	82.2	94	228
HPRCC08	939490	901	blastx.14	2.19 [Homo sapiens]	gi 854082 emb CAA6	54%	120	296

HPWAS77	908450	914	HMMER 2.1.1	PFAM: gag gene protein p24 (core nucleocapsid protein)	0645.1  PF00607	92.3	655	266
			blastx.14	gag protein [Human endogenous retrovirus K]	gi 1780975 emb CAA 71418.1	37% 38% 45% 50%	730 185 253 25	248 108 188 2
HSWAC73	710354	926	HMMER 1.8	PFAM: WD domain, G- beta repeats	PF00400	9.99	134	190
HTEAL28	963538	939	blastx.14	(AL080154) hypothetical protein [Homo sapiens]	gi 5262611 emb CAB 45745.1	36%	234	413
HTEBC74	887782	945	HMMER 1.8	PFAM: Armadillo segment protein, repeats	PF00514	20.2	58	183
HTEBY08	960427	954	HMMER 2.1.1	PFAM: Protein phosphatase 2A regulatory subunit PR55	PF01240	92.8	63	251
			blastx.14	protein phosphatase 2A1 B gamma subunit [Oryctolagus cuniculus]	gi 619215 gb AAA58 956.1	97% 87%	63 231	197 254
HTECA21	911369	962	HMMER 2.1.1	PFAM: PDZ domain (Also known as DHR or GLGF)	PF00595	57.6	100	354
			blastx.14	tyrosine phosphatase [Homo sapiens]	gi 1486367 emb CAA 56124.1	57% 51%	85 467	351 652
HTEDI02	921243	994	HMMER 2.1.1	PFAM: Leucine Rich Repeat	PF00560	36.2	346	414
			blastx.14	densin-180 [Rattus norvegicus]	gi 1657758 gb AAC5 2881.1	36% 32%	220 214	450 450

HTEDQ30	530589	1007	HMMER 2.1.1	PFAM: Ferritins	PF00210	34% 30% 33% 26% 29% 36% 36% 24% 26% 40% 29% 29% 31% 29% 24%	220 241 214 214 214 268 463 220 214 463 463 463 463 463 463	456 450 453 441 450 450 612 453 453 588 606 606 606 603 612
HTEDU48	932315	1013	blastx.14	(AF176069) ubiquilin [Homo sapiens]	g 5733824 gb AAD4 9751.1 AF176069_1	66% 46% 55% 57% 24% 28% 26% 15% 24% 32% 25%	11 305 587 452 251 293 332 311 569 184 329	118 454 688 535 472 388 502 490 679 267 436
HTEDY38	771505	1017	HMMER	PFAM: Zinc-binding	PF00099	2.19	9	44

HTEHY54	922964	1018	1.8 blastx.14	metalloprotease domain lysozyme [Gallus gallus]	gi 63426 emb CAA43 319.1	46% 41% 61% 65.2	696 405 234 93	457 220 181 197
HTEGGM38	675087	1059	HMMER 2.1.1	PFAM: DnaJ domain	PF00226			
HTEGO05	932583	1061	HMMER 2.1.1 blastx.14	PFAM: Eukaryotic protein kinase domain male germ cell-associated kinase (mak) [Rattus norvegicus]	PF00069 gi 205278 gb AAA41 562.1	50.8 85% 64% 85% 38%	3 3 489 768 1023	233 395 761 848 1100
HTEHC47	973071	1085	blastx.2	unnamed protein product [unidentified]	emb CAB42447.1	29%	112	612
HTEHI14	526687	1096	HMMER 2.1.1	PFAM: lactate/malate dehydrogenase	PF00056	50.6	222	371
HTEHS19	529280	1113	HMMER 2.1.1	PFAM: 7 transmembrane receptor (Secretin family)	PF00002	19.3	16	135
HTEHV72	920610	1117	HMMER 2.1.1	PFAM: IQ calmodulin- binding motif	PF00612	41.7	178	240
HTEIB14	963099	1127	HMMER 2.1.1 blastx.14	PFAM: Zinc finger, C2H2 type Bowel [Drosophila melanogaster]	PF00096 gi 388166 gb AAB1 7949.1	53.9 90% 33% 80% 33% 46% 28% 31%	78 9 9 227 9 9 54 230	146 236 230 316 230 149 230 334

HTEIF40	958355	1128	blastx.14	(AF132972) CGI-38 protein [Homo sapiens]	gi 4680715 gb AAD2 7747.1 AF132972.1	35%	224	316
HTEIK11	967431	1136	blastx.14	Zfp-29 [Mus musculus]	gi 55471 emb CAA38 920.1	28%	188	367
						50%	353	406
						50%	353	406
						50%	353	406
						50%	353	406
						44%	353	406
						61%	368	406
						47%	356	406
						42%	60	137
						38%	353	406
						44%	356	409
						100%	411	431
						85%	411	431
						85%	411	431
						87%	408	431
						100%	414	431
HTEIL07	953803	1139	HMMER 1.8	PFAM: EF hand	PF00036	11.27	192	263
HTEIP88	941155	1148	HMMER 2.1.1	PFAM: Transmembrane amino acid transporter protein	PF01490	34.7	1	216
HTEIU92	870652	1154	HMMER 2.1.1	PFAM: Transketolase	PF00456	70.1	1	225

HTEIV54	922027	1155	blastx.14	p18H-rev 107 [Rattus norvegicus]	gi 433963 emb CAA53991.1	40%	359	682
HTEIY80	955242	1163	blastx.14	(AF146793) protein B [Mus musculus]	gi 4836805 gb AAD30564.1 AF146793_1	65%	251	364
HTEJE15	908360	1170	HMMER 1.8	PFAM: Helicases conserved C-terminal domain	PF00271	91%	320	454
			blastx.14	vasa-like gene protein, RVLG protein=putative DEAD 1 [Rattus sp.]	gi 806464 gb AAB33364.1	74%	453	569
HTEJF45	942476	1172	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	83%	111	203
			blastx.2	(AB017800) nolp [Homo sapiens]	dbj BAA34576.1	31%	257	322
HTEJP10	914785	1180	HMMER 1.8	PFAM: Heat shock hsp90 proteins	PF00183	14.92	5	52
HTEJP66	916481	1181	blastx.14	(AF151885) CGI-127 protein [Homo sapiens]	gi 4929723 gb AAD34122.1 AF151885_1	73%	2	190
HTEKS20	846714	1210	HMMER 2.1.1	PFAM: EF hand	PF00036	84%	242	319
HTELE10	963563	1221	blastx.14	integumentary mucin B.1 [Xenopus laevis]	gi 1184035 emb CAA64795.1	65%	188	265
HTELJ89	966134	1229	HMMER 1.8	PFAM: Zinc-binding metalloprotease domain	PF00099	2.28	593	637
HTELV86	910946	1252	HMMER	PFAM: Fibronectin type	PF00041	69%	135	299
						53%	290	487
						77%	523	549
						37%	540	629
						13.29	110	214
						100%	499	639
						62%	626	706
						84.7	453	539
						75%	339	244
						2.6	290	316
						77.22	400	669

[illegible]



HTEMP49	932319	1280	blastx.14	(AL117564) hypothetical protein [Homo sapiens]	gi 5912114 emb CAB55995.1	42% 58%	134 43	78 8
HTEMR65	909280	1281	HMMER 2.1.1 blastx.2	PFAM: Zinc finger, C2H2 type zinc finger protein [Homo sapiens]	PF00096 emb CAA55533.1	91% 51.5%	12 35	629 103
HTEMT06	934338	1284	blastx.14	120 kDa style glycoprotein [Nicotiana glauca]	gi 2653671 gb AAC15893.1	61% 56% 56% 54% 52% 50% 53% 51% 51% 53% 51% 52% 51% 40% 45%	2 2 2 2 2 2 2 2 2 5 2 5 2 909 866	286 286 286 292 286 304 286 286 286 286 283 286 283 998 931
HTEMX92	913795	1288	HMMER 2.1.1 blastx.14	PFAM: BTB/POZ domain (AF086831) leukemia/lymphoma related factor cLRF	PF00651 gi 3599513 gb AAC35368.1	28% 37% 32% 62.3%	50 240 80 122	280 383 226 319
						47% 32%	143 331	337 450

HTENI58	917213	1299	HMMER 2.1.1 blastx.14	[Gallus gallus] PFAM: HMG (high mobility group) box	PF00505	118.2	308	514
				HMG-X protein [Xenopus laevis]	gi 639691 dbj BAA06 440.1	43% 43% 26% 57%	269 101 89 446	514 319 214 487
HTENP54	787535	1306	HMMER 1.8	PFAM: Bacterial regulatory proteins, luxR family	PF00196	6.37	107	199
HTENP80	775387	1307	HMMER 1.8	PFAM: TPR Domain	PF00515	11.77	83	166
HTENR10	963530	1309	blastx.14	protein kinase related to Raf protein kinases; 1	gi 1171248 gb AAC5 0354.1	82%	10	132
HTENR93	920834	1311	blastx.14	(AF121781) unknown [Homo sapiens]	gi 4210989 gb AAD1 2066.1	79% 74%	285 620	644 808
HTENY35	884043	1319	HMMER 1.8	PFAM: Zinc finger, C3HC4 type (RING finger)	PF00097	6.56	449	592
HTEOF80	847224	1327	HMMER 1.8	PFAM: EGF-like domain	PF00008	14.65	20	100
HTEOI36	870575	1330	HMMER 1.8	PFAM: HMG (high mobility group) box	PF00505	15.44	69	236
HTEON29	815852	1333	HMMER 1.8	PFAM: EF hand	PF00036	22.29	266	349
HTEOV90	870532	1336	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	11.37	358	435
HTEOW39	870566	1338	HMMER 1.8	PFAM: C-type lysozymes and alpha-lactalbumin	PF00062	126.92	59	295

HTEPA08	958391	1340	blastx.14	(AF004430) hD54+ins2 isoform [Homo sapiens]	gi 2895085 gb AAC98478.1	47%	225	482
HTEPE28	932576	1347	HMMER 2.1.1	PFAM: metalloproteinase family M24	PF00557	67%	483	575
			blastx.14	(AC002387) putative methionine aminopeptidase [Arabidopsis thaliana]	gi 2583129 gb AAB82638.1	203	2	442
HTEPM33	870561	1354	HMMER 2.1.1	PFAM: LIM domain containing proteins	PF00412	68%	4	180
HTEPN07	952243	1356	blastx.14	WW domain binding protein-2 [Homo sapiens]	gi 4205086 gb AAD10951.1	54%	174	311
			blastx.14	(AF081947) tektin [Mus musculus]	gi 4235350 gb AAD13183.1	42%	9	158
HTEPV02	917406	1366	HMMER 2.1.1	PFAM: Ank repeat	PF00023	73%	30	689
			blastx.14	alt. ankyrin (variant 2.2) [Homo sapiens]	gi 747710 emb CAA34611.1	21%	72	590
HTEPX32	870698	1367	HMMER 1.8	PFAM: Double-stranded RNA binding motif	PF00035	30.4	343	435
HTEQD40	915198	1371	blastx.14	(AC004877) sco-spondin-mucin-like; similar to P98167 1 sapiens]	gi 3638957 gb AAC36301.1	41%	247	411
						36	508	699
HTEQE87	958354	1373	blastx.14	(AF132972) CGI-38 protein [Homo sapiens]	gi 4680715 gb AAD27747.1 AF132972.1	30%	278	171
						33%	266	195
						43%	188	141
						45%	506	447
						54%	110	78
						42%	121	65
						25%	260	177
						50%	334	645
						58%	149	349

HTEQP45	966141	1379	HMMER 1.8	PFAM: HMG (high mobility group) box	PF00505	5.99	7	48
HTEQR15	939641	1381	HMMER 1.8	PFAM: 4 transmembrane segments integral membrane proteins	PF00335	32.9	174	455
HTEQT63	924799	1383	blastx.2	(AF133424) tetraspanin TM4-B [Homo sapiens]	gb AAAF08363.1 AF1 33424.1	74%	141	698
HTLCA95	911655	1398	HMMER 2.1.1	PFAM: Bacterial mutT protein	PF00293	3.53	472	501
			HMMER 2.1.1	PFAM: Actin	PF00022	345.2	170	1096
			blastx.14	actin 2 [Echinococcus granulosus]	gi 290399 gb AAC80 574.1	50% 42% 53% 45% 63%	170 761 677 593 2	568 1096 760 652 34
HTLCY54	908832	1402	HMMER 2.1.1	PFAM: DnaJ domain	PF00226	119.8	245	445
			blastx.14	(AB014888) MRJ [Homo sapiens]	gi 3402485 dbj BAA3 2209.1	67% 78% 47% 40%	239 797 632 611	616 934 694 691
HTLDE64	908613	1407	HMMER 2.1.1	PFAM: Zinc finger, C2H2 type	PF00096	47.6	197	271
			blastx.2	Kruppel-like factor LKLF [Mus musculus]	gb AAA86728.1	61% 42%	179 57	355 176
HTLDF33	909254	1409	HMMER 2.1.1	PFAM: Zinc finger, C2H2 type	PF00096	80.8	51	119
			blastx.2	(AL022067) dJ134E15.1	emb CAB36862.1	70%	12	422

HTLDG55	911645	1410	blastx.14	(Blimp-1) [Homo sapiens] actin [Trypanosoma brucei]	gi 161963 gb AAA30 151.1	38%	24	392
HTLDO94	915223	1413	blastx.14	(AC004667) hypothetical protein [Arabidopsis thaliana]	gi 3668087 gb AAC6 1819.1	37% 34% 37% 44% 30% 38% 29%	96 108 108 40 37 40 43	263 263 242 93 105 93 93
HTLDS55	891322	1416	HMMER 2.1.1	PFAM: Cell division protein	PF00735	454.7	233	1069
			blastx.2	(AJ250723) septin-like protein Sint1 [Mus musculus]	emb CAB59833.1	63%	131	1054
HTLDT05	909752	1417	HMMER 2.1.1	PFAM: PH domain	PF00169	36.9	59	271
			blastx.2	(AK000004) FLJ00004 protein [Homo sapiens]	dbj BAA92229.1	77%	47	487
HTLDU05	911649	1419	HMMER 1.8	PFAM: Actins	PF00022	141.45	125	469
			blastx.14	(AF113908) actin-related protein [Emericella nidulans]	gi 4731565 gb AAD2 8502.1 AF113908_1	30% 33%	2 451	469 540
HTLEH30	934287	1429	blastx.14	(AF025310) tssk-1 and tssk-2 kinase substrate [Mus musculus]	gi 2739052 gb AAC0 3366.1	90% 58% 81%	205 343 306	270 429 338
HTLEJ11	973302	1431	HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF00069	55.9	44	223

HTLET56	911654	1444	blastx.14 HMMER 1.8	(AF144573) Mx- interacting protein kinase PKM [Mesocricetus auratus] PFAM: Actins	gi 4868443 gb AAD3 1319.1 AF144573_1	69% 40% 42% 38%	35 437 293 877	268 592 397 939
					PF00022	262.03	134	703
			blastx.14	actin [Filobasidiella neoformans]	gi 508701 gb AAC49 074.1	52% 33% 53% 52%	143 787 721 966	715 963 804 1022
HTLET78	836820	1445	HMMER 2.1.1	PFAM: Proprotein convertase P-domain	PF01483	216.9	38	433
HTLEV95	883332	1448	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	1.97	172	225
HTLEY11	967309	1451	blastx.14	(AC004877) sco-spondin- mucin-like; similar to P98167 1 sapiens]	gi 3638957 gb AAC3 6301.1	66%	267	250
HTLFE05	954984	1459	blastx.14	(AJ007798) nuclear protein SA3 [Homo sapiens]	gi 5834580 emb CAB 55312.1	86% 65%	12 589	731 924
HTLFI39	953730	1462	blastx.2	(AF053356) ORF4 [Homo sapiens]	gb AAC78801.1	100% 100% 100%	77 3 376	256 77 420
HTLGD25	870136	1465	HMMER 1.8	PFAM: Ubiquitin family	PF00240	83.86	79	324
HTLGM07	952254	1470	HMMER 2.1.1	PFAM: 'Cold-shock' DNA-binding domain	PF00313	70.2	3	158
			blastx.14	(AF096834) germ cell	gi 4837737 gb AAD3	90%	3	323

HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	100%	393	485
						100%	549	614
						100%	711	761
HTLGT62	918606	1471	blastx.14	a6(IV) collagen [Homo sapiens]	gi 1850097 dbj BAA09791.1	36%	661	750
						28%	637	720
						34%	117	203
						40%	475	519
						63%	487	519
						48%	187	261
						38%	379	456
						61%	503	541
						40%	113	178
						80%	232	261
HTLGT62	918606	1471	blastx.14	a6(IV) collagen [Homo sapiens]	gi 1850097 dbj BAA09791.1	61%	181	219
						53%	229	273
						37%	196	276
						42%	14	70
						66%	181	207
						20.1	637	846
						36.8	9	95
HTLGT62	918606	1471	blastx.14	a6(IV) collagen [Homo sapiens]	gi 1850097 dbj BAA09791.1	88%	3	260
						92%	330	443
						62%	424	528
						100%	539	577
						37%	539	625
HTLGT62	918606	1471	blastx.14	a6(IV) collagen [Homo sapiens]	gi 1850097 dbj BAA09791.1	34%	397	483
						50%	519	572
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	100%	393	485
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	100%	549	614
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	100%	711	761
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	36%	661	750
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	28%	637	720
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	34%	117	203
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	40%	475	519
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	63%	487	519
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	48%	187	261
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	38%	379	456
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	61%	503	541
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	40%	113	178
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	80%	232	261
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	61%	181	219
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	53%	229	273
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	37%	196	276
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	42%	14	70
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	66%	181	207
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	20.1	637	846
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	36.8	9	95
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	88%	3	260
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	92%	330	443
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	62%	424	528
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	100%	539	577
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	37%	539	625
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	34%	397	483
HTLGT62	918606	1471	blastx.14	specific Y-box binding protein [Homo sapiens]	0662.1	50%	519	572

HTLHP32	933335	1478	HMMER 1.8	PFAM: RNA recognition motif. (aka RRM, RBD, or RNP domain)	PF00076	70% 28% 23% 34% 37% 30% 30%	584 509 342 54 460 256 402	613 634 479 140 531 363 479
HTLHT15	946586	1481	blastx.14	(AL032626) cDNA EST EMBL:D70654 comes from this 1 1 1 yk377b8.3 comes f	gi 3925211 emb CAA 21539.1	43% 66% 50% 58% 39%	1 287 402 235 240	243 358 455 270 308
HTLHV67	936139	1484	blastx.14	(AF005038) secretory carrier membrane protein [Homo sapiens]	gi 5230678 gb AAB6 2723.2	83% 60% 96% 66%	152 591 465 2	475 749 542 46
HTLHZ10	963475	1486	blastx.14	circumsporozoite protein [Plasmodium vivax]	gi 482882 gb AAC46 499.1	37% 35% 33% 35% 45% 45% 45% 40% 50% 50%	3 3 3 45 128 181 234 128 234 340	137 137 137 137 187 240 293 187 281 387



HTLJD36	945891	1488	blastx.2	(AC004410) fos39554_1 [Homo sapiens]			40%	181	240
							40%	128	187
							40%	128	187
							50%	287	334
							50%	287	334
							40%	234	293
							40%	128	187
							40%	181	240
							50%	234	281
							50%	340	387
							40%	287	346
							50%	128	175
							50%	258	293
							50%	205	240
							50%	311	346
							54%	6	275
							71%	292	417
							57%	257	319
HTLIY52	942161	1495	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF000069		251.19	166	933
			blastx.2	serine/threonine kinase [Mus musculus]	gb AAA99535.1		44%	133	936
HTLJA23	953729	1496	blastx.2	(AF053356) ORF4 [Homo sapiens]	gb AAC78801.1		100%	2	274
							100%	394	438
HTLJC71	922923	1498	HMMER 1.8	PFAM: Src homology domain 3	PF00018		9.14	1152	1340
			blastx.2	(AL133030) hypothetical protein [Homo sapiens]	emb CAB61362.1		94%	3	1355
HTLJD88	953714	1500	blastx.14	(AF025310) tssk-1 and	gi 2739052 gb AAC0		83%	3	206

				tssk-2 kinase substrate [Mus musculus]	3366.1		74% 95% 72% 77% 63% 32% 60%	554 263 516 468 510 260 21	715 391 548 494 542 334 50
HTLJJ75	924755	1501	HMMER 2.1.1 blastx.14	PFAM: Coenzyme A transferase succinyl-CoA:alpha- ketoacid coenzyme A transferase [Sus scrofa]	PF01144		317.7	445	813
HTTBJ94	530564	1515	HMMER 2.1.1	PFAM: Protein of unknown function	PF01871		63.2	18	254
HTTCT34	973210	1521	HMMER 2.1.1 blastx.2	PFAM: Divalent cation transporter (AK000480) unnamed protein product [Homo sapiens]	PF01769		46.7	93	251
HTTDO19	908937	1532	HMMER 2.1.1 blastx.2	PFAM: Zinc finger, C2H2 type zinc finger protein [Homo sapiens]	PF00096		42.8	22	90
					emb CAA55529.1		76% 72% 45% 67% 44% 67% 50%	1 1 1 1 1 1 13	129 129 237 129 237 129 234

HTTEU68	967819	1543	blastx.14	glycosyl-phosphatidyl- inositol-anchored protein homolog [Mus musculus]	gi 1098569 gb AAA8 2599.1	63% 36% 71% 90% 36% 36% 57% 50%	125 180 149 161 180 180 180 180	190 287 190 190 287 287 221 227
HTTFM66	950051	1556	blastx.2	(AK001269) unnamed protein product [Homo sapiens]	dbj BAA91592.1	36% 52% 32% 52% 43% 84%	26 536 197 759 377 195	190 649 352 827 424 1124
HTTKP07	911390	1587	HMMER 1.8 blastx.2	PFAM: Src homology domain 3 (AL049683) hypothetical protein [Homo sapiens]	PF00018 emb CAB41255.1	15.82 51% 56%	47 8 292	196 289 450
HUKAC72	966804	1594	blastx.14	DARPP-32=DOPAMINE AND CAMP- REGULATED PHOSPHOPROTEIN.	sp G545790 G545790	81%	73	309
HUVCQ07	928053	1612	blastx.14	SHB=SRC HOMOLOG 2 PROTEIN.	sp G545100 G545100	44% 52% 6.83	102 6 282	251 68 323
HUVFH03	922064	1639	HMMER 1.8	PFAM: FAD/NAD- binding domain in oxidoreductases	PF00175			

HUVGZ77	909169	1650	HMMER 2.1.1	PFAM: BTB/POZ domain	PF00651	51.2	110	253
			blastx.14	(AB011665) BAZF [Mus musculus]	gi 3287501 dbj BAA31223.1	94% 87%	47 295	301 366
HUVHC93	908555	1653	HMMER 2.1.1	PFAM: KRAB box	PF01352	152.7	147	335
			blastx.14	ha0946 protein is Kruppel-related. [Homo sapiens]	gi 498152 dbj BAA06541.1	64% 55%	135 72	362 131
HVCAZ38	969208	1659	blastx.2	(AK000496) unnamed protein product [Homo sapiens]	dbj BAA91205.1	64% 75%	395 151	159 110
HVVBK72	933167	1668	HMMER 1.8	PFAM: UDP-glucoronosyl and UDP-glucosyl transferases	PF00201	70.01	2	391
HWLHJ68	957834	1671	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	6.35	216	278
			blastx.14	(AB012265) wizL [Mus musculus]	gi 3551182 dbj BAA32790.1	55% 39%	201 101	314 169
HVVBY08	957658	1673	HMMER 2.1.1	PFAM: Sm protein	PF01423	79.4	134	355
			blastx.14	(AC005258) R30783_1 [Homo sapiens]	gi 3289993 gb AAC25622.1	97% 100%	185 130	403 195
HUVGP05	930892	1677	blastx.14	(AF091457) zinc finger protein RIN ZF [Rattus norvegicus]	gi 4557143 gb AAD22522.1 AF091457_1	82% 100%	231 217	398 246
HUVFI01	945834	1679	blastx.2	similar to human TRAMP protein. [Homo sapiens]	dbj BAA06540.1	98%	103	1212
HUNAF20	961527	1693	blastx.14	(AF184971) cytokine	gi 6013325 gb AAF01	100%	382	278

HUNAE02	921132	1696	blastx.14	receptor homolog 1 (AF151848) CGI-90 protein. [Homo sapiens]	320.1 AF184971.1	100%	2	94
HUKEP18	957456	1710	HMMER 1.8	PFAM: Trypsin	gi 4929649 gb AAD3 4085.1 AF151848.1	82.96	729	361
HUKDG10	968333	1713	blastx.2	(AF100707) testes- specific protein TSP50 [Homo sapiens]	gb AAF22500.1 AF1 00707.1	100%	118	588
HTTJN26	869612	1744	blastx.14	F35D2.4 gene product [Caenorhabditis elegans]	gi 861294 gb AAA68 328.1	47%	3	314
HTTIR04	926772	1748	blastx.2	cDNA EST yk38f6.5 comes from this gene; cDNA EST EMBL:D75296 comes from this gene [Caenorhabditis elegans]	emb CAB04553.1	35% 50%	587 666	345 589
HTTDM42	460948	1762	blastx.14	(AF092091) cp431 [Rattus norvegicus]	gi 3851160 gb AAC7 2234.1	45% 26%	462 195	163 118
HTTBP62	932997	1771	HMMER 2.1.1	PFAM: KRAB box	PF01352	79.1	282	401
HTLHK57	946914	2662	blastx.14	(AF036705) Similar to phytoene desaturase; coded for 1 1 1 coded for acetylcholine receptor alpha 9 subunit [Rattus rattus]	gi 2749982 gb AAB9 5172.1	69% 68%	64 373	336 468
HTLHB93	945862	1797	blastx.2	(AJ006692) ultra high sulfur keratin [Homo sapiens]	gi 595481 gb AAA56 720.1	76% 71%	783 586	938 720
					emb CAA07188.1	40% 39%	21 21	272 272

HTLGS10	963458	1799	blastx.14	pro-alpha-2(I) collagen [Mus musculus]	gi 50489 emb CAA41 205.1	34%	108	212
						50%	380	433
HTLEQ92	932882	1804	blastx.14	(AL117444) hypothetical protein [Homo sapiens]	gi 5911890 emb CAB 55929.1	26%	186	320
						53%	302	340
HTLEN77	772363	1806	HMMER 1.8	PFAM: EF hand	PF00036	100%	6	107
						100%	203	256
HTLDZ81	778180	1810	HMMER 1.8	PFAM: Tubulin	PF00091	36%	213	269
						26.93	294	380
HTLDW27	961353	1811	blastx.14	(AF014461) EXO70 protein [Mus musculus]	gi 2352998 gb AAB6 9345.1	12.29	156	245
						95%	239	601
						100%	186	236
						88%	76	126
						76%	1	51
						63%	36	68
HTLBH67	751985	1821	HMMER 1.8	PFAM: Src homology domain 3	PF00018	37.78	16	162
HTFBE02	920507	1830	HMMER 2.1.1	PFAM: Isopentenyl- diphosphate delta- isomerase	PF01772	95.6	103	291
HTEQN83	908528	1834	HMMER 2.1.1	PFAM: KRAB box	PF01352	98.7	81	203
			blastx.14	(AL080125) hypothetical protein [Homo sapiens]	gi 5262560 emb CAB 45723.1	62%	75	251
						66%	39	74
HTEPE35	948475	1838	HMMER 2.1.1	PFAM: Phosphatidylinositol- specific phospholipase C, Y domain	PF00387	163.8	839	507

				blastx.2	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase 1	pir S14113 S14113	48%	1	750
HTEOY82	948845	1839		blastx.14	(AJ010949) calcium channel alpha-2-delta-C subunit [Mus musculus]	gi 4186073 emb CAA09423.1	97%	165	374
HTEMV66	813038	1852		HMMER 2.1.1	PFAM: Eukaryotic protein kinase domain	PF00069	27.8	154	315
HTEMU66	944419	1853		HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	114.85	613	963
				blastx.2	MEK Kinase 3 [Mus musculus]	gb AAB03535.1	49%	604	948
HTEMO58	964769	1855		blastx.14	casein kinase 1 gamma 1 isoform [Rattus norvegicus]	gi 854733 gb AAC52200.1	82%	395	195
							65%	482	423
							87%	424	401
							77%	214	188
HTEKH17	942526	1867		blastx.2	(AF016184) putative pheromone receptor [Rattus norvegicus]	gb AAC33331.1	70%	300	88
							53%	602	378
							52%	85	29
HTEGJ74	765901	1892		HMMER 2.1.1	PFAM: Tudor domain	PF00567	38.5	6	167
HTEDH90	909165	1924		HMMER 2.1.1	PFAM: BTB/POZ domain	PF00651	38.1	195	308
				blastx.14	(AF097916) HIV-1 inducer of short transcripts binding protein [Homo sapiens]	gi 3860089 gb AAC72973.1	45%	150	308
							39%	348	416
HTEDH42	615250	1926		HMMER 2.1.1	PFAM: ADP-ribosylation factor family	PF00025	156.4	42	353

HTEDF22	908406	1935	HMMER 1.8 blastx.2	PFAM: Zinc finger, CCHC class nucleic acid binding protein [Mus sp.]	PF00098	20.37	250	297
HTECC09	678659	1952	HMMER 1.8 blastx.2	PFAM: Zinc finger, C3HC4 type (RING finger)	gb AA89198.1	46%	52	303
HPWTA06	936026	1982	HMMER 1.8 blastx.14	(AF151048) HSPC214 [Homo sapiens] Collagenase precursor (EC 3.4.-.-). [Escherichia coli]	PF00097	14.18	261	338
HPWSA52	727294	1983	HMMER 1.8	PFAM: Homeobox domain	gb AAF36134.1 AF1 51048.1	85%	111	332
HPWAJ39	575271	1993	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	gi 1742347 dbj BAA1 5068.1	100% 100% 100% 58% 64%	624 359 457 216 169	454 207 362 115 86
HPRAG45	939849	2672	HMMER 1.8	PFAM: WD domain, G- beta repeats	PF00400	21.65	135	212
HPMGR15	660374	2040	HMMER 1.8	PFAM: Phorbol esters / diacylglycerol binding domain	PF00130	2.84	307	333
HPLAI10	968707	2074	blastx.14	AT motif-binding factor [Mus musculus]	gi 1345408 dbj BAA0 5046.1	33%	443	496
HPJEV95	929723	2076	HMMER 1.8	PFAM: ATP synthase A chain	PF00119	20.61	169	393
HPJDT03	922815	2083	HMMER	PFAM: WW/rsp5/WWP	PF00397	9.71	294	371



HPJDA25	951281	2087	1.8 blastx.2	domain containing proteins (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	gb AAD15748.1	73%	291	488
HPJDA25	951284	2676	blastx.14	(AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	gi 4321407 gb AAD1 5748.1	87%	219	97
HPJDAQ70	973604	2130	HMMER 1.8 blastx.14	PFAM: Flagella basal body rod proteins Flagellar hook-associated protein 1 (hap1) . [Escherichia coli]	PF00460	41.51	206	298
HPCTD03	922149	2191	HMMER 2.1.1 blastx.14	PFAM: Pterin 4 alpha carbinolamine dehydratase pterin-4a-carbinolamine dehydratase [Homo sapiens]	gi 1651528 dbj BAA3 5891.1	77% 100%	322 194	498 322
HPCOV68	911075	2195	blastx.14	(AC004500) GDF-9 [Homo sapiens]	PF01329	143.1	6	305
HPCAO89	946913	2196	HMMER 1.8 blastx.2	PFAM: Serpins (serine protease inhibitors) leupin [Homo sapiens]	gi 848985 gb AAA69 662.1	62%	18	311
HOVEE20	909030	2207	HMMER 2.1.1 blastx.14	PFAM: KRAB box zinc finger protein 30 [Mus musculus]	gi 2996640 gb AAC0 8450.1	64%	2	160
					PF00079	53.12	94	309
					emb CAA61420.1	39% 45%	82 309	327 452
					PF01352	105.4	229	348
					gi 456269 emb CAA8 2913.1	67% 33%	193 367	348 429

HOVCO50	932544	2211	HMMER 1.8 blastx.14	domesticus] PFAM: Zinc-binding metalloprotease domain (AF072860) protein activator of the 1	PF00099 gi 3290198 gb AAC2 5672.1	2.22	464	508
HOOKF04	925784	2244	blastx.14	(AF092091) cp431 [Rattus norvegicus]	gi 3851160 gb AAC7 2234.1	82% 43%	458 204	577 251
HOOJN04	925783	2246	blastx.14	(AF011336) putative E1- E2 ATPase [Mus musculus]	gi 2944187 gb AAC0 5245.1	94% 94% 29% 27% 100%	2 158 5 5 4	157 265 127 115 153
HONAD02	859016	2261	HMMER 2.1.1	PFAM: Polyprenyl synthetases	PF00348	38.5	753	905
HOGAM56	908904	2276	blastx.14	ZINC FINGER [CLONE ZNF78L1].	sp G299838 G299838	63% 68% 56% 50% 46%	6 3 33 188 191	179 152 176 235 235
HOFNW65	815822	2286	HMMER 2.1.1	PFAM: Calpain family cysteine protease	PF00648	34.2	18	89
HOFNW07	953436	2288	HMMER 2.1.1 blastx.14	PFAM: Cytochrome c/c1 heme lyase holocytochrome c-type synthetase [Homo sapiens]	PF01265 gi 1209635 gb AAB1 9007.1	21.1	259	354
HOFNI10	964682	2301	blastx.14	similar to Human zinc- finger protein, BR140(P1:JC2069)	gi 1504012 dbj BAA1 3205.1	71% 83%	190 139	360 192
						100% 90% 100%	150 64 271	269 153 291

HOFNC80	835718	2303	HMMER 1.8	[Homo sapiens] PFAM: IG (immunoglobulin) superfamily	PF00047	66%	293	319
			blastx	(AF111714) junctional adhesion molecule [Bos taurus]	gb AAD42051.1 AF1 11714_1	71% 94% 33%	28 306 306	303 362 359
HOFMT55	888552	2311	HMMER 2.1.1	PFAM: Caspase recruitment domain	PF00619	43	111	239
HOFMS43	947973	2313	HMMER 2.1.1	PFAM: Sushi domain (SCR repeat)	PF00084	64	174	302
			blastx.2	porcine membrane cofactor protein [Sus scrofa]	dbj BAA20476.1	47%	12	317
HOFMP09	943358	2315	HMMER 2.1.1	PFAM: Immunoglobulin domain	PF00047	27.5	34	144
			blastx	B-CAM [Homo sapiens]	emb CAA56327.1	76% 49% 85% 33% 46% 43%	31 300 473 247 283 91	351 494 553 372 327 138
HOFMF82	693987	2317	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	10.91	44	106
HOFMF82	694062	2688	HMMER 2.1.1	PFAM: Zinc finger, C2H2 type	PF00096	53.7	372	440
HOFMF82	909248	2689	HMMER 2.1.1	PFAM: Zinc finger, C2H2 type	PF00096	48.3	61	129
			blastx.14	zinc finger protein [Homo]	gi 495568 gb AAC50	52%	19	429

HOF25	942367	2320	blastx.2	sapiens]	264.1]	50%	55	429
				(AF036696) contains similarity to Brassica oleracea non-green 1 (GB:U13632) [Caenorhabditis elegans]	gb AAB88349.1	39%	289	969
HODFF88	974911	2341	HMMER 1.8	PFAM: Eukaryotic protein kinase domain	PF00069	101.43	98	370
			blastx.14	mixed-lineage protein kinase 1 - human	pir S32467 JU0229	74%	131	493
						81%	763	921
						30%	751	915
HODFD73	909812	2343	HMMER 2.1.1	PFAM: GTPase-activator protein for Ras-like GTPase	PF00616	34	190	390
			blastx.14	(AB016962) synGAP-b1 [Rattus norvegicus]	gi 4417207 dbj BAA74972.1	98%	4	480
HODCZ64	745966	2357	blastx.2	elastin like protein [Drosophila melanogaster]	emb CAA59990.1	75%	3	86
						42%	364	405
						42%	358	399
HODAK55	745532	2383	HMMER 1.8	PFAM: ATPases associated with various cellular activities (AAA)	PF00004	60.69	11	157
HOCPH02	917453	2400	HMMER 1.8	PFAM: Zinc finger, C3HC4 type (RING finger)	PF00097	8.27	265	309
HNIAB26	974750	2412	blastx.14	PR-1-like protein	gi 166861 gb AAA32	37%	388	143

HLWFB01	915399	2419	blastx.14	[Arabidopsis thaliana] (AL117637) hypothetical protein [Homo sapiens]	863.1 gi 5912226 emb CAB 56026.1	94%	155	328
HLWBC21	869611	2443	HMMER 1.8	PFAM: Src homology domain 3	PF00018	3.29	350	379
HLWBA27	931387	2445	blastx.14	(AF070657) glutathione S-transferase subunit 13 homolog [Homo sapiens]	gi 4454690 gb AAD2 0963.1	93% 75% 100%	89 486 277	286 533 306
HLWAW86	941397	2692	HMMER 1.8	PFAM: Integrins alpha chain	PF00357	163.29	115	459
HLWAR08	959139	2448	HMMER 1.8	PFAM: Ank repeat	PF00023	13.97	3	44
HLWAL31	971312	2693	HMMER 2.1.1 blastx.2	PFAM: Leucine rich repeat C-terminal domain (AF133270) SLIT2 [Homo sapiens]	PF01463 gb AAD25539.1 AF1 33270_1	51.7 89% 37% 35% 30% 72% 57%	317 77 77 92 92 495 493	466 565 481 505 553 524 534
HIMAU07	961623	2466	blastx.14	(AB016088) RNA binding protein [Homo sapiens]	gi 5821145 dbj BAA8 3714.1	75%	321	1
HETLF29	909762	2471	HMMER 1.8 blastx.14	PFAM: Eukaryotic protein kinase domain similar to cAMP- dependant protein kinase; cDNA EST 111	PF00069 gi 3878636 emb CAA 88953.1	143.18 56%	6 6	416 416
HETBE61	965638	2483	blastx.14	(AF151833) CGI-75 protein [Homo sapiens]	gi 4929619 gb AAD3 4070.1 AF151833_1	88% 77%	347 247	526 339

HEQCC01	924849	2488	blastx.14	(AF151878) CGL-120 protein [Homo sapiens]	gi 4929709 gb AAD34115.1 AF151878_1	93% 81%	318 215	365 262
HEQBG85	827915	2492	HMMER 1.8	PFAM: Peroxidases	PF00141	73% 69%	892 343	422 266
HEQAD73	914044	2500	blastx.14	(AL023286) hypothetical protein [Schizosaccharomyces pombe]	gi 3116115 emb CAA18866.1	24.44	13	162
HEPCB04	941270	2502	blastx.14	(AF153605) androgen induced protein [Homo sapiens]	gi 5231135 gb AAD41087.1 AF153605_1	38% 39% 70%	319 463 203	444 546 232
HEPAJ04	933091	2513	blastx.14	(AL034368) predicted using hexExon; L779.3; 1	gi 4760337 emb CAB39078.2	97%	524	387
HEGBC03	922550	2516	blastx.14	similar to collagen [Caenorhabditis elegans]	gi 3873667 emb CAA94874.1	44% 87% 50% 50% 45%	95 302 201 1 230	148 325 236 42 262
HEEAX09	912065	2525	HMMER 1.8	PFAM: lipocalins	PF00061	57% 66%	252 229	293 255
HEEAG51	930810	2533	blastx.14	epididymal secretory protein I (ESP I) [Rattus norvegicus]	gi 56117 emb CAA42493.1	12.2	86	205
HCOMM05	925952	2554	HMMER 1.8	(AF083108) sirtuin type 3 [Homo sapiens] PFAM: Src homology domain 3	gi 5225322 gb AAD40851.1 AF083108_1 PF00018	39% 39% 33% 82% 75% 59.48	86 8 206 94 260 178	208 76 259 282 295 342

HCHOX63	957690	2556	blastx.14	epidermal growth factor receptor kinase substrate [Homo sapiens]	gb AAA62280.1	46% 43% 23%	445 115 43	840 435 222
HCHNW48	862478	2557	HMMER 1.8	CDC42 GTPase- activating protein [Homo sapiens]	gi 409027 gb AAA16 142.1	64% 78%	112 661	597 702
HCHMW18	966985	2559	blastx.14	PFAM: Laminin B (Domain IV)	PF00052	1.52	230	289
HCHMI15	935298	2562	blastx.14	(AB017614) OASIS protein [Mus musculus]	gi 4519621 dbj BAA7 5670.1	100% 68% 39%	538 440 308	386 222 240
HCHAI62	743411	2570	HMMER 1.8	PSD-95/SAP90-associated protein-4 [Rattus norvegicus]	gi 1864093 gb AAB4 8590.1	52% 75% 91% 50%	181 682 584 620	582 825 691 667
HCDMC22	672815	2578	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	8.45	2	76
HBGTT76	903653	2619	HMMER 2.1.1	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	9.49	182	241
HBGMT82	954374	2624	blastx.14	PFAM: Ank repeat	PF00023	62.3	197	295
HBGDF39	861602	2631	HMMER	(AJ133120) Proline rich synapse associated protein 2 [Rattus norvegicus]	gi 5262748 emb CAB 45688.1	72% 47%	131 499	556 561
			blastx.14	(AJ004801) very large virion protein (tegument) [Bovine herpesvirus type 1.1]	gi 265331 emb CAA 06097.1	37% 35% 32%	187 91 91	267 201 201
			HMMER	PFAM: Response	PF00072	44.82	158	355

HBCPV80	932817	2639	1.8 HMMER 2.1.1	regulator receiver domain PFAM: WW domain	PF00397	64.2	71	160
HAQCD07	958959	2649	blastx.14	(AC005581) R31237_1, partial CDS [Homo sapiens]	gi 3510234 gb AAC3 3487.1	100%	1	108



[075] Table 2 further characterizes certain encoded polypeptides of the invention, by providing the results of comparisons to protein and protein family databases. The first column provides a unique clone identifier, "Clone ID NO:", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" which allows correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide sequences. The fourth column provides the analysis method by which the homology/identity disclosed in the row was determined. The fifth column provides a description of PFam/NR hits having significant matches identified by each analysis. Column six provides the accession number of the PFam/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in column five. Comparisons were made between polypeptides encoded by polynucleotides of the invention and a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFam"), as described below.

[076] The NR database, which comprises the NBRF PIR database, the NCBI GenPept database, and the SIB SwissProt and TrEMBL databases, was made non-redundant using the computer program nrdb2 (Warren Gish, Washington University in Saint Louis). Each of the polynucleotides shown in Table 1A, column 3 (e.g., SEQ ID NO:X or the 'Query' sequence) was used to search against the NR database. The computer program BLASTX was used to compare a 6-frame translation of the Query sequence to the NR database (for information about the BLASTX algorithm please see Altshul et al., J. Mol. Biol. 215:403-410 (1990), and Gish et al., Nat. Genet. 3:266-272 (1993)). A description of the sequence that is most similar to the Query sequence (the highest scoring 'Subject') is shown in column five of Table 2 and the database accession number for that sequence is provided in column six. The highest scoring 'Subject' is reported in Table 2 if (a) the estimated probability that the match occurred by chance alone is less than  $1.0e-07$ , and (b) the match was not to a known repetitive element. BLASTX returns alignments of short polypeptide segments of the Query and Subject sequences which share a high degree of similarity; these segments are known as High-Scoring Segment Pairs or HSPs. Table 2 reports the degree of similarity

between the Query and the Subject for each HSP as a percent identity in Column 7. The percent identity is determined by dividing the number of exact matches between the two aligned sequences in the HSP, dividing by the number of Query amino acids in the HSP and multiplying by 100. The polynucleotides of SEQ ID NO:X which encode the polypeptide sequence that generates an HSP are delineated by columns 8 and 9 of Table 2.

[077] The PFam database, PFam version 5.2, (Sonnhammer et al., Nucl. Acids Res., 26:320-322, (1998)) consists of a series of multiple sequence alignments; one alignment for each protein family. Each multiple sequence alignment is converted into a probability model called a Hidden Markov Model, or HMM, that represents the position-specific variation among the sequences that make up the multiple sequence alignment (see, e.g., R. Durbin et al., *Biological sequence analysis: probabilistic models of proteins and nucleic acids*, Cambridge University Press, 1998 for the theory of HMMs). The program HMMER version 1.8 (Sean Eddy, Washington University in Saint Louis) was used to compare the predicted protein sequence for each Query sequence (SEQ ID NO:Y in Table 1A) to each of the HMMs derived from PFam version 5.2. A HMM derived from PFam version 5.2 was said to be a significant match to a polypeptide of the invention if the score returned by HMMER 1.8 was greater than 0.8 times the HMMER 1.8 score obtained with the most distantly related known member of that protein family. The description of the PFam family which shares a significant match with a polypeptide of the invention is listed in column 5 of Table 2, and the database accession number of the PFam hit is provided in column 6. Column 7 provides the score returned by HMMER version 1.8 for the alignment. Columns 8 and 9 delineate the polynucleotides of SEQ ID NO:X which encode the polypeptide sequence which shows a significant match to a PFam protein family.

[078] As mentioned, columns 8 and 9 in Table 2, "NT From" and "NT To", delineate the polynucleotides of "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFam/NR database as disclosed in the fifth column of Table 2. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the polynucleotides of SEQ ID NO:X delineated in columns 8 and 9 of Table 2. Also provided are polynucleotides encoding such proteins, and the complementary strand thereto.

- [079] The nucleotide sequence SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, the nucleotide sequences of SEQ ID NO:X are useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in Clone ID NO:Z. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing, and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to these polypeptides, or fragments thereof, and/or to the polypeptides encoded by the cDNA clones identified in, for example, Table 1A.
- [080] Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).
- [081] Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, and a predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing cDNA Clone ID NO:Z (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, 6 and 7). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.

[082] The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

***RACE Protocol For Recovery of Full-Length Genes***

[083] Partial cDNA clones can be made full-length by utilizing the rapid amplification of cDNA ends (RACE) procedure described in Frohman, M.A., et al., Proc. Nat'l. Acad. Sci. USA, 85:8998-9002 (1988). A cDNA clone missing either the 5' or 3' end can be reconstructed to include the absent base pairs extending to the translational start or stop codon, respectively. In some cases, cDNAs are missing the start codon of translation. The following briefly describes a modification of this original 5' RACE procedure. Poly A+ or total RNA is reverse transcribed with Superscript II (Gibco/BRL) and an antisense or complementary primer specific to the cDNA sequence. The primer is removed from the reaction with a Microcon Concentrator (Amicon). The first-strand cDNA is then tailed with dATP and terminal deoxynucleotide transferase (Gibco/BRL). Thus, an anchor sequence is produced which is needed for PCR amplification. The second strand is synthesized from the dA-tail in PCR buffer, Taq DNA polymerase (Perkin-Elmer Cetus), an oligo-dT primer containing three adjacent restriction sites (XhoI, SalI and ClaI) at the 5' end and a primer containing just these restriction sites. This double-stranded cDNA is PCR amplified for 40 cycles with the same primers as well as a nested cDNA-specific antisense primer. The PCR products are size-separated on an ethidium bromide-agarose gel and the region of gel containing cDNA products the predicted size of missing protein-coding DNA is removed. cDNA is purified from the agarose with the Magic PCR Prep kit (Promega), restriction digested with XhoI or SalI, and ligated to a plasmid such as pBluescript SKII (Stratagene) at XhoI and EcoRV sites. This DNA is transformed into bacteria and the plasmid clones sequenced to identify the correct protein-coding inserts. Correct 5' ends are confirmed by comparing this sequence with the putatively identified homologue and overlap with the partial cDNA clone. Similar

methods known in the art and/or commercial kits are used to amplify and recover 3' ends.

[084] Several quality-controlled kits are commercially available for purchase. Similar reagents and methods to those above are supplied in kit form from Gibco/BRL for both 5' and 3' RACE for recovery of full length genes. A second kit is available from Clontech which is a modification of a related technique, SLIC (single-stranded ligation to single-stranded cDNA), developed by Dumas et al., *Nucleic Acids Res.*, 19:5227-32 (1991). The major differences in procedure are that the RNA is alkaline hydrolyzed after reverse transcription and RNA ligase is used to join a restriction site-containing anchor primer to the first-strand cDNA. This obviates the necessity for the dA-tailing reaction which results in a polyT stretch that is difficult to sequence past.

[085] An alternative to generating 5' or 3' cDNA from RNA is to use cDNA library double-stranded DNA. An asymmetric PCR-amplified antisense cDNA strand is synthesized with an antisense cDNA-specific primer and a plasmid-anchored primer. These primers are removed and a symmetric PCR reaction is performed with a nested cDNA-specific antisense primer and the plasmid-anchored primer.

***RNA Ligase Protocol For Generating The 5' or 3' End Sequences To Obtain Full Length Genes***

[086] Once a gene of interest is identified, several methods are available for the identification of the 5' or 3' portions of the gene which may not be present in the original cDNA plasmid. These methods include, but are not limited to, filter probing, clone enrichment using specific probes and protocols similar and identical to 5' and 3' RACE. While the full length gene may be present in the library and can be identified by probing, a useful method for generating the 5' or 3' end is to use the existing sequence information from the original cDNA to generate the missing information. A method similar to 5' RACE is available for generating the missing 5' end of a desired full-length gene. (This method was published by Fromont-Racine et al., *Nucleic Acids Res.*, 21(7):1683-1684 (1993)). Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcript. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest, is

used to PCR amplify the 5' portion of the desired full length gene which may then be sequenced and used to generate the full length gene. This method starts with total RNA isolated from the desired source, poly A RNA may be used but is not a prerequisite for this procedure. The RNA preparation may then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase, if used, is then inactivated and the RNA is treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase. This modified RNA preparation can then be used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction can then be used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the reproductive system antigen of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the relevant reproductive system antigen.

[087] The present invention also relates to vectors or plasmids, which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, 6 and 7) is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as shown, for example, in Table 7. These deposits are referred to as "the deposits" herein. The tissues from which some of the clones were derived are listed in Table 7, and the vector in which the corresponding cDNA is contained is also indicated in Table 7. The deposited material includes cDNA clones corresponding to SEQ ID NO:X described, for example, in Table 1A (Clone ID NO:Z). A clone which is isolatable from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X, may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Furthermore,

although the sequence listing may in some instances list only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to sequence the DNA included in a clone contained in the ATCC Deposits by use of a sequence (or portion thereof) described in, for example Tables 1A or 2 by procedures hereinafter further described, and others apparent to those skilled in the art.

[088] Also provided in Table 7 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for convenience.

[089] Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128,256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., *Nucleic Acids Res.* 16:7583-7600 (1988); Altting-Mees, M. A. and Short, J. M., *Nucleic Acids Res.* 17:9494 (1989)) and pBK (Altting-Mees, M. A. et al., *Strategies* 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into *E. coli* strain XL-1 Blue, also available from Stratagene.

[090] Vectors pSport1, pCMVSPORT 1.0, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus* 15:59- (1993). Vector lafmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR<sup>®</sup>2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nuc. Acids Res.* 16:9677-9686 (1988) and Mead, D. et al., *Bio/Technology* 9: (1991).

- [091] The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the deposited clone (Clone ID NO:Z). The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.
- [092] Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of reproductive system associated genes corresponding to SEQ ID NO:X or the complement thereof, polypeptides encoded by SEQ ID NO:X or the complement thereof, and/or the cDNA contained in Clone ID NO:Z, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.
- [093] The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.
- [094] The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.
- [095] The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988).



Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the reproductive system polypeptides of the present invention in methods which are well known in the art.

[096] The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA sequence contained in Clone ID NO:Z. The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X or a complement thereof, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or the polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, a polypeptide encoded by the cDNA contained in Clone ID NO:Z and/or a polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, a nucleic acid sequence encoding a polypeptide encoded by the complement of the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA contained in Clone ID NO:Z.

[097] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in Table 1B column 6, or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides

of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[098] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different

from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[099] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (See Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and

variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[0100] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. In preferred embodiments, the polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, wherein sequentially delineated sequences in the table (i.e. corresponding to those exons located closest to each other) are directly contiguous in a 5' to 3' orientation. In further embodiments, above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[0101] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B, and the

polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1B, column 2) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[0102] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same Clone ID NO:Z. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[0103] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same row of column 6 of Table 1B. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[0104] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-

described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[0105] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[0106] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[0107] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or

alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides, are also encompassed by the invention.

[0108] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[0109] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same Clone ID NO:Z (see Table 1B, column 1) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[0110] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one sequence in column 6 corresponding to the same contig sequence identifier

SEQ ID NO:X (see Table 1B, column 2) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[0111] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same row are directly contiguous. In preferred embodiments, the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B is directly contiguous with the 5' 10 polynucleotides of the next sequential exon delineated in Table 1B, column 6. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[0112] Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. Accordingly, for each contig sequence (SEQ ID NO:X) listed in the third column of Table 1A, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, b is an integer of 15 to the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions



of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to  $a + 14$ . More specifically, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a and b are integers as defined in columns 4 and 5, respectively, of Table 3. In specific embodiments, the polynucleotides of the invention do not consist of at least one, two, three, four, five, ten, or more of the specific polynucleotide sequences referenced by the Genbank Accession No. as disclosed in column 6 of Table 3 (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone). In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example. All references available through these accessions are hereby incorporated by reference in their entirety.

**TABLE 3**

Clone ID NO: Z	SEQ ID NO: X	Contig ID:	EST Disclaimer Range of a Range of b	Accession #'s
H7MCE35	11	928554	1 - 59	15 - 73
H7MDC49	12	722780	1 - 148	15 - 162
H7MDD72	13	847688	1 - 592	15 - 606
HAOSH55	14	952380	1 - 694	15 - 708
				AI139000, AA884996, AA889649, and AA724461. AW182856, AI218191, AA834537, AA804628, AA827835, AF034780, and E07989. AI681511, AA677498, AI799484, AI360937, AI378075, AI457270, AI363333, AI681227, AI806180, AI363339, AA972313, AA627925, AI984311, AA483815, N25951, AI250808, AI417147, AW297301, AI079688, AW009637, AI289263, AA768395, AA769533, AW085089, AW368116, AW067835, AI110587, N26848, W15533, AI129095, AW298190, AI300955, AI870137, AW410019, AI808400, AA748383, AA479673, AW269239, AA281561, AA807144, AW291197, AW373450, and N42781. H93040, H93056, AA719305, AA808945, AI342677, AA742815, AC006581, AP000045, AP000113, AC007684, AC002404, AC003070, AC003042, AP000327, AC003043, AC005829, AB023048, AP000123, AP000170, AP000055, AC007066, AC002350, AC005399, AI135744, AC005031, AF001549, AC004913, Z95114, AL031663, AL008729, Z97054, AL133355, AC000381, AC005207, AC009516, U80017, Z81370, AC006023, AC006449, AC005296, AC005069, AC000118, AC004821, AC006146, AC005037, AC006441, AL109798, AL031432, AL080243, AC004819, AL109627, AC002477, and AC004882.
HAQAK73	15	764671	1 - 728	15 - 742
HAQAM17	16	664979	1 - 347	15 - 361
HAQBF84	17	783259	1 - 56	15 - 70
HAQBJ71	18	839982	1 - 409	15 - 423
HAQBQ50	19	522004	1 - 83	15 - 97
HAQBS37	20	847519	1 - 710	15 - 724
HAUBD69	21	529711	1 - 121	15 - 135
HAUBU10	22	968339	1 - 324	15 - 338
HBC/S08	23	957826	1 - 492	15 - 506
				AW419224, AW419225, and AW419223. AL119483, AA809125, AL119444, AA835346, AA188940, AC016027, AC016830, AC005529, AC005261, AC004531, AC005255, AC006137, AC006080, AL049874, AL132777, L44140, AL031983, AC006515, AC004659, Z85987, AC005531, AF134726, AC006441, AC004858, AF053356, AP000552, AC005740, AP000503, AC012627, AC004882, AC003108, AC007934, AL049758, AC005181, AF109907, AC004033, AC005091, AC007685, AC005971, AC003663, AC005274, AC005089, AL049829, AC006449, U96629, AC004973, AL049872, AC007283, AC005057, AC004231, AL035413, AL078638, AC006023, AC005815, AL031311, AL023803, AC005821, AL049780, AL031228, AC005919, AP000555, AL049631, AC004895, AC005072, AC005736, AL021155, AL022165, AL133448, AL133245, AC007055, AL008718, AC004526,

						AC007065, AL049776, U07563, AL035681, AP000114, AP000046, AF205588, AC005231, AC005841, AC004491, AC007193, AC007878, AL031591, AF038458, AL049869, AC012384, AC003002, AL133485, AL109984, AC004983, AL121653, AC005049, AC005839, AC002418, AC004386, D84401, AC003037, AC002091, AL049538, AC002070, AF045555, Z93244, AC006468, AL022316, AC006141, AC004854, AC005067, AC005768, AC007993, AL008719, AC004522, AC004099, AC006512, AC005088, AC004884, AL031427, AD000092, AC005624, AL109758, Z70281, AC004859, AC005081, AL079295, AC002425, AB026898, AC004985, AL035072, AC005484, AC004816, AC005914, AL121754, AC004890, AC005746, AL121757, Z86090, AL109627, AL133163, AC000003, AC009721, Z82250, AC007057, and AC005071.
HBCPD14	24	963634	1 - 127	15 - 141		
HBCQJ03	25	922401	1 - 124	15 - 138	AW392670, Z99396, AL119319, AL036418, AL036858, AW372827, AW384394, AL119457, AL119483, AL119324, AW363220, AL119484, AL119391, AL119497, AL119522, U46351, AL119418, AL119355, AL119443, AL119363, AL037094, AL119341, U46341, AL134902, AL119396, U46349, AL119401, U46350, U46347, AL042551, AL037205, AL119335, AL119496, AL119439, AL134536, AL036196, AL037082, AL119444, AL134525, AL036268, U46346, AL038837, AL042614, AL134920, AL043019, AL042984, AL037051, AL042965, AL042975, AL036725, AL042544, AA631969, AL119399, AL134538, U46345, AL042542, AL043029, AL042450, AL043003, AL036924, AL037526, AL119464, AR066494, AR060234, A81671, AB026436, AD001527, AR054110, AR023813, AR064707, and AR069079.	
HBCQS90	26	951787	1 - 507	15 - 521	AA191298, AW364854, AI205727, R16601, and AI188004.	
HBCQS93	27	930682	1 - 607	15 - 621	AA703200, W88470, and Z39990.	
HGBGD28	28	525846	1 - 314	15 - 328		
HGBGF56	29	957870	1 - 240	15 - 254		
HGBBG42	30	922396	1 - 689	15 - 703	N33183, AA169202, AI393342, AW172574, AA731731, AI961101, AA872188, W17122, AI219418, AA609341, AA485152, AW293905, AI221103, AI910881, AW195626, AA856740, AA767183, AW072218, AA929018, AI338682, AA836394, AA448345, AW293908, AI264116, W26762, AA766127, AA761418, H30745, AA315954, AI022328, AI032738, AI203338, AI768542, AI979322, AA470714, AA303837, AA992529, AA764904, AA627584, AA769119, AA169659, AI217749, W70324, AA333338, AI250852, AI635634, AI147877, AI382313, AI377000, AI520946, AI955310, AL036241, AI638523, AI589668, AA814517, AA001397, AI096773, AF122922, and Y14314.	
HGBBH43	31	524532	1 - 183	15 - 197	AI863446, AI188331, AW014913, AI073437, AW291378, AI130693, AI768987, and AA890464.	
HGBBS07	32	954299	1 - 403	15 - 417	AA229977, N41881, N23545, H78888, H54240, AW270016, and AA569612.	
HGBBT79	33	525352	1 - 318	15 - 332		
HGBBW60	34	954916	1 - 555	15 - 569	AI808278, AI697307, AI936570, AW167940, AI379188, AI669686, AI751739, AW450137,	

						AI868311, AI203915, AW182104, AW014255, AI766481, AI821507, AA548667, AI194990, AF061970, U81600, and X52875.
HGBBW72	35	524956	1 - 321	15 - 335		
HBGDA44	36	525618	1 - 493	15 - 507		
HBGDE85	37	524875	1 - 125	15 - 139		
HBGDS13	38	971696	1 - 245	15 - 259		
HBGDT43	39	974223	1 - 433	15 - 447		AI567076, AW270343, AA169263, AW275510, AI801482, AA362511, AI933534, AA847499, AA580808, AA226363, AA502104, AI311927, AA569471, AL042753, AL048925, AA502860, AI133297, AI499588, AW021583, AA531079, AW248819, F25733, AW341900, AA101689, R86151, AA494102, AA482923, AA715255, AA715267, AA516222, AA758934, AI783494, AA602047, AI751216, AA664909, T60681, AA320966, AL119691, AA428792, AA828042, AI445674, AW062724, AA493695, AW302013, AA469451, AI281881, AW193461, AI919265, AA484679, AA632612, AI085719, AA601202, AA653375, AA491862, AA713891, AI687343, AA491650, AI584186, AA468456, AA757775, AW438643, AL036037, AA577959, AI873990, AA568869, AA515334, AA668807, AA508359, AI872020, AW023990, AA643455, AI282511, AA658362, AA724333, H73082, AI538870, AW073060, AA908687, AA487621, AA493621, AA620467, AI471887, AI368256, AI240168, AI345157, AL038705, AA683238, AI568678, H71429, AA662225, AA470969, AI797903, AA488746, AA719292, AA846952, AA804925, AW084466, F27407, AA837791, AI589461, AA747594, AI933299, AI564454, AI924872, AA572713, AI708139, AA490183, AA019312, AI583283, AI054343, AL042547, AW274349, AA811153, AA446544, F17555, AA368059, AW050498, AI338350, AA478355, AA773472, AA634889, AA502155, AA665021, AI247199, AI559251, R02632, AA484373, AW050734, AW235497, R40056, AW193265, AW273218, AW021207, AI472222, AA633753, AW408047, AW303196, AI350211, AW301809, AA668639, AA584581, AA573725, AW247819, AI669453, AA805846, T06754, T09071, AA623002, AW104030, AA806796, AA773902, AA577906, AI625647, AA515909, AI521679, AW302903, AA483223, AI801600, AA581903, AW075948, AI692808, AA503600, AI284640, AI589230, AI744995, AI860013, AW407578, AA629874, AW327868, AI702314, AA181823, AA704009, AA189117, AA743716, AL135377, AL044858, AI859742, AA179944, AI110844, AI110770, AW300625, AI754658, AL119984, AI354388, AI285576, AI873852, AI903462, AA487417, N64587, AW131155, AW301350, AA578861, AA493708, AW196064, AI241821, AL119166, T74382, AI807762, AI381253, AA828767, AI656840, AA501615, AA758366, AL078634, U82671, AP000569, AP000301, AC006255, AP000114, AP000045, AC005668, AC007556, AC007878, AC005191, AF085954, AC005089, AC005261, AL133276, U67827, X75335, AC006571, Z68278, AF039906, AL022320, AI049758, AC007286, AC012599, AC004230, AC002310, AC005385, U62317, Z97053, AC004112, AL022316, AC010200, AC002091, AL031283, AF107885, AC005284, AC005406,